

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2004, 15:21:38 ; Search time 17 Seconds
(without alignments)

891.319 Million cell updates/sec

Title: US-09-936-845A-15

Perfect score: 1545
Sequence: 1 MELAEFWNDLNTFTYGNPH.....PFVKAYIIKSKSKSVKNE 291

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1545	100.0	291	YLPA_CABEL	Q03574 caenorhabdi
2	564	36.5	435	YYS_CABEL	P49191 caenorhabdi
3	492	31.8	270	ELO3_HUMAN	Q9H803 homo sapien
4	479	31.0	271	ELO3_MOUSE	Q35949 mus musculu
5	263.5	17.1	312	ELO4_MOUSE	Q9EGC4 mus musculu
6	262	17.0	345	ELO3_YEAST	P40319 saccharomyc
7	261	16.9	314	ELO4_MACFA	Q95K73 macaca fasc
8	254	16.4	314	ELO4_HUMAN	Q9GXR5 homo sapien
9	239.5	15.5	279	ELO1_MOUSE	Q9JJJ5 mus musculu
10	239	15.5	279	ELO1_HUMAN	Q9BW60 homo sapien
11	220.5	14.3	310	ELO1_YEAST	P39540 saccharomyc
12	220	14.2	347	ELO2_YEAST	P25358 saccharomyc
13	219	14.2	282	ELO2_MOUSE	Q9JJJ4 mus musculu
14	214	13.9	286	ELO2_HUMAN	Q9NB29 homo sapien
15	102	6.6	880	YE21_ARCFU	O28851 archaeoglob
16	99.5	6.4	919	YK05_YEAST	P36051 saccharomyc
17	97.5	6.3	498	TLCA_RICPR	P19568 rickettsia
18	96.5	6.2	392	OLSF_DROME	Q9VHE6 drosophila
19	96	6.2	473	NOR8_PSEST	P98008 pseudomonas
20	95	6.1	359	E124_HUMAN	O14681 homo sapien
21	93	6.1	2671	IP3T_HUMAN	Q14573 homo sapien
22	93.5	6.1	759	NAHS_ONCMY	Q01345 oncorhynch
23	92	6.0	526	ALG8_HUMAN	Q9BWK2 homo sapien
24	91.5	5.9	289	Y771_ARCFU	O29487 archaeoglob
25	91.5	5.9	317	O6N2_HUMAN	Q8NGY6 homo sapien
26	91.5	5.9	503	ALG6_CABEL	Q09326 caenorhabdi
27	91.5	5.9	629	CTR1_HUMAN	P30825 homo sapien
28	91	5.9	591	FZD9_HUMAN	O00144 homo sapien
29	91	5.9	873	SYA_WIGER	Q8DZW8 wigleswort
30	90.5	5.9	466	NOR8_PSEAE	Q59647 pseudomonas
31	90	5.8	466	GAC2_RAT	P18508 rattus norv
32	90	5.8	474	GAC2_MOUSE	P22723 mus musculu
33	89.5	5.8	295	LPLC_BACSU	P39129 bacillus su

ALIGNMENTS

RESULT 1

YLPA_CABEL
ID YLPA_CABEL STANDARD; PRT; 291 AA.

AC Q03574;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Hypothetical 34.1 kDa protein C40H1.4 in chromosome III.

GN C40H1.4

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Pelodierinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RX MEDLINE=94150718; PubMed=7906398;

RA Wilson K., Ainscough R., Anderson K., Baynes C., Berks M., Cooper J., Coulson A.,

RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fraser A.,

RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,

RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,

RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,

RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,

RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkhen R.,

RA Sims M., Smallon N., Smith A., Smith M., Sonhammer E., Staden R.,

RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,

RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,

RA Wohldman P.;

RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

RT elegans.";

RL Nature 368:32-38(1994)

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -!- SIMILARITY: Belongs to the ELO family.

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CC EMBL; Z19154; CAA79555.1; -

DR PIR; S28299; S28299.

DR WormPep; C40H1.4; CE00112.

DR InterPro; IPR002076; GNS1_SUR4.

DR Pfam; PF01151; ELO; 1.

DR Prosite; PS01188; ELO; 1.

DR Hypothetical protein; Transmembrane.

FT TRANSMEM 46 66 POTENTIAL.

FT TRANSMEM 79 99 POTENTIAL.

FT TRANSMEM 254 274 POTENTIAL.

SQ SEQUENCE 291 AA; 34059 MW; 6657272A53B343F CRC64;

Query Match 100.0%; Score 1545; DB 1; Length 291;

Best Local Similarity 100.0%; Pred. No. 4.3e-121;

P18794 streptococc
P21548 gallus gall
Q91194 mus musculu
P51533 saccharomyc
O52535 klebsiella
P98059 rhodobacter
Q61070 mus musculu
P35855 lactobacill
P18507 homo sapien
P34322 caenorhabdi
Q92415 rickettsia
Q92670 zymomonas m

Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 XELAEFNDLNTFIYGNTHDMTKYKYSVHPGEQVADPOYNTILFQKYWHSITISV 60
 DB 1 XELAEFNDLNTFIYGNTHDMTKYKYSVHPGEQVADPOYNTILFQKYWHSITISV 60
 QY 61 LYFILLIKVIOKFMENRKPFTLKYPILLWNGALAAFSIIATLRFSDIDPLSLYAEGFYKTL 120
 DB 61 LYFILLIKVIOKFMENRKPFTLKYPILLWNGALAAFSIIATLRFSDIDPLSLYAEGFYKTL 120
 QY 121 CYSNPTDVAAPFSAFALSIVELGDTNFIILKRPLIFLHYHHAANVLIYVHSGAEH 180
 DB 121 CYSNPTDVAAPFSAFALSIVELGDTNFIILKRPLIFLHYHHAANVLIYVHSGAEH 180
 QY 181 TAAGRFYILNYPFAHSLMYTYVTSANGYRLPKWVSMVTVTQTTOMLAGVGITWVYKV 240
 DB 181 TAAGRFYILNYPFAHSLMYTYVTSANGYRLPKWVSMVTVTQTTOMLAGVGITWVYKV 240
 QY 241 KTEYKLPCCQSVANLYLAFVIYVTFALLFTQFPVKAVIIKSSKSKSVKNE 291
 DB 241 KTEYKLPCCQSVANLYLAFVIYVTFALLFTQFPVKAVIIKSSKSKSVKNE 291

RESULT 2
 YFS3_CABEL STANDARD; PRT; 435 AA.
 AC P49191;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical 51.5 kDa protein D2024.3 in chromosome IV.
 GN D2024.3
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Du Z., Gattung S.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- SIMILARITY: Belongs to the ELO family.
 CC
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 CC
 CC EMBL; U41011; AAA82288.1; -;
 DR PIR; T34200; T34200.
 DR WormPep; D2024.3; CE04292.
 DR InterPro; IPR002076; GNS1_SUR4.
 DR Pfam; PF01151; ELO; 1.
 DR PROSITE; PS01188; ELO; 1.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 42 62 POTENTIAL.
 FT TRANSMEM 103 123 POTENTIAL.
 FT TRANSMEM 239 259 POTENTIAL.
 FT TRANSMEM 278 298 POTENTIAL.
 SQ SEQUENCE 435 AA; 5148 MW; F7940A74A1969914 CRC64;

Query Match 36.5%; Score 564; DB 1; Length 435;
 Best Local Similarity 42.0%; Pred No. 1.4e-39;
 Matches 128; Conservative 45; Mismatches 56; Indels 46; Gaps 7;

QY 22 DMTTKY---KYSHHPGEQVADPOYNTILFQKYWHSITISVYFILI-----KVI----- 69
 DB 5 DYNPKYGLNYSIELPFETSPDPRSTWQNHVYQISITASVYVAVIFTKGVVLIYKK 64

QY 70 -----QKF--MENRKPFTLKYPILLWNGALAAFSIIATL 102
 DB 65 SRVITPESSLOAKNENKSLNSQFOMEKYPFOLDTELFVWNSFLAIFSILGFLR 124
 QY 103 FSIDPLRSIYARG--FYKTLCYSCNPTDVAAPFSAFALSIVELGDTNFIILKRPLIP 160
 DB 125 MTEPEFVWSASAGNSFKYSICHSSYAQGVGTGFWTFQFAMSKLPELIDITIPVLRKPLIP 184
 QY 161 LHYHYHAAVLIYVHSGAEHTAAGRFYILNYPFAHSLMYTYVTSANGYRLPKWVSMVTY 220
 DB 185 LKWYHHTVWYVTHAYKDHDTASGRFWIMWYGVHVALMYSYALRSLSKLPKQAMVVT 244
 QY 221 TVQTTOMLAGVGITWVYKVT--EYKLPCCQSVANLYLAFVIYVTFALLFTQFPVKAVI 278
 DB 245 TLQLAQMGMVGIIGTVTVRIKSSGEY---CQQTWNLGLCPGVYFYFILLPANFFYHAYV 301
 QY 279 IKSSK 283
 DB 302 KKNR 306

RESULT 3
 ELO3_HUMAN STANDARD; PRT; 270 AA.
 ID ELO3_HUMAN
 AC Q9H803; Q8N180;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Elongation of very long chain fatty acids protein 3 (Cold inducible
 DE glycoprotein of 30 kDa).
 GN ELOVL3 OR CIG30.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buesow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., McWhan P.J., McKernan K.J., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywicki M.I., Skalska U., Smalius D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.;
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE OF 35-270 FROM N.A.
 RA Semina E.V., Murray J.C.;
 RT "The CIG30/PITX3/GDF1 gene configuration is conserved between human
 RT and mouse genomes.";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: May be involved in a membrane event related to cellular
 CC proliferation in brown adipose tissue. Could be implicated in
 CC synthesis of very long chain fatty acids and sphingolipids. May
 CC catalyze one or both of the reduction reaction in fatty acid
 CC elongation, i.e., conversion of beta-ketoacyl CoA to beta-
 CC hydroxyacyl CoA or reduction of trans-2-enoyl CoA to the saturated
 CC acyl CoA derivative (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic

```
CC reticulum (Potential).
CC -!- SIMILARITY: Belongs to the ELO family.
CC -----
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CC -----
DR ENBL; BC034344; AAI34344.1; -.
DR ENBL; AF292387; AAG17875.1; -.
DR Gene; HGNC:18047; ELOVL3.
DR InterPro; IPR002076; GNS1_SUR4.
DR Pfam; PF01151; ELO; 1.
DR PROSITE; PS01188; ELO; 1.
KM Fatty acid biosynthesis; Transmembrane; Endoplasmic reticulum.
FT TRANSMEM 29 49
FT TRANSMEM 66 86
FT TRANSMEM 164 186
FT TRANSMEM 198 218
FT TRANSMEM 235 255
FT SITE 266 268
FT SITE ENDOPLASMIC RETICULUM RETRIEVAL MOTIF
FT SITE (POTENTIAL).
SQ SEQUENCE 270 AA; 31500 MW; 0C6C8F1E7B5DE8B1 CRC64;
Query Match 31.8%; Score 492; DB 1; Length 270;
Best Local Similarity 39.9%; Pred. No. 7.7e-34;
Matches 97; Conservative 53; Mismatches 87; Indels 6; Gaps 3;
QY 48 PQYVHSTISVLYILIKVIOKFNENKPFLLKYPLILWNGALAAFSIATLRESIDP 107
DB 30 FEYWATSPDIAIYIVLLAVGQNYKRGKGFNLQGLPILMSCLAFISLGAVRWGM 89
QY 108 LRSVLAEGFYKILCY-SCNPTDVAAFWSFAPALSKIVELGDTMFIILRKPLIFLYHH 166
DB 90 GTVLLTGELKQVCFINFDNSVTKFSWVFLLSKVIELGDTAFIILRKPLIFHYHH 149
QY 167 AAVLIIVTSGAEHTAAGRFYILMNVFALSIXTYTVTSAMGVRILPKWVSVTVTTQ 226
DB 150 STVLVTVTFQYKKNKVPAGGFVTFMGVFAIKTYTYTLKAANKVKKPMLPLITSQ 209
QY 227 MLAGVGITVMVYKVEYKLPCCOOSVANLYLAFVIYTVTALPIQPFVXAYI---IKSK 283
DB 210 MFGAIVSILTYIWRQDQ--GCHTWEHLFWSPILMTWFIILFAHFCQYIRPKYAKT 267
QY 284 KSK 286
DB 268 KSQ 270
RESULT 4
ID ELO3_MOUSE STANDARD; PRT; 271 AA.
AC Q35949;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Elongation of very long chain fatty acids protein 3 (Cold inducible
DE Glycoprotein of 30 kDa) (CIN-2).
GN ELOVL3 OR CIG30.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brown adipose tissue;
RX MEDLINE=98058971; PubMed=9395518;
RA Tvrdik P., Asadi A., Kozak L.P., Nedergaard J., Cannon B.,
RA Jacobsson A.;
RA "Cig30, a mouse member of a novel membrane protein gene family, is
involved in the recruitment of brown adipose tissue.";
J. Biol. Chem. 272:31738-31746 (1997).
[2]
SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RX MEDLINE=99403085; PubMed=10473596;
RA Tvrdik P., Asadi A., Kozak L.P., Nuglozeh E., Parente P.,
RA Nedergaard J., Jacobsson A.;
RA "Cig30 and Pdx3 genes are arranged in a partially overlapping
RA tail-to-tail array resulting in complementary transcripts.";
J. Biol. Chem. 274:26387-26392 (1999).
[3]
SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loguillano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length
RA human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
-!- FUNCTION: May be involved in a membrane event related to cellular
proliferation in brown adipose tissue. Could be implicated in
synthesis of very long chain fatty acids and sphingolipids. May
catalyze one or both of the reduction reaction in fatty acid
elongation, i.e., conversion of beta-ketoacyl CoA to beta-
hydroxyacyl CoA or reduction of trans-2-enoyl CoA to the saturated
acyl CoA derivative.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
reticulum (Potential).
-!- TISSUE SPECIFICITY: Readily detected in brown adipose tissue and
liver. Weak expression in kidney, white adipose tissue, heart and
skin. Not detected in lung, testis, muscle, spleen, brain, thymus
and intestine.
-!- INDUCTION: Elevated in brown adipose tissue in conditions of brown
fat recruitment, namely cold stress, perinatal development and
after diet-induced thermogenesis. A synergistic action of both
catecholamines and glucocorticoids is required for the induction.
-!- SIMILARITY: Belongs to the ELO family.
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EMBL; U97107; AAC06127.1; -.
EMBL; AF054504; AAD51088.1; -.
EMBL; BC016468; AAI16468.1; -.
MGD; MGI:1195976; Elov13.
InterPro; IPR002076; GNS1_SUR4.
Pfam; PF01151; ELO; 1.
PROSITE; PS01188; ELO; 1.
Fatty acid biosynthesis; Transmembrane; Endoplasmic reticulum;
Glycoprotein.
TRANSMEM 30 50
TRANSMEM 67 87
POTENTIAL.
POTENTIAL.
```


RA MEDLINE=94299524; PubMed=8027068;
RA Garcia-Arreaza M., Maldonado A.M., Mazon M.J., Portillo F.;
RT "Transcriptional control of yeast plasma membrane H(+)-ATPase by
RT glucose. Cloning and characterization of a new gene involved in this
RT regulation.";
RN J. Biol. Chem. 269:18076-18082(1994).
RN [4]
RC SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=97313267; PubMed=9169871;
RA Johnston M., Hillier L., Riles L., Albermann K., Andre B., Anson W.,
RA Barnes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A.,
RA Etian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K.,
RA Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P.,
RA Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moesl D.,
RA Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,
RA Portetle D., Purnelle B., Reckmann S., Rieger M., Rinke M., Rose M.,
RA Schaefer M., Scherens B., Scholler P., Schwager C., Schwarz S.,
RA Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P.,
RA Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,
RA Medler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
RL Nature 387:87-90(1997).
RN [5]
RN SEQUENCE FROM N.A.
RX MEDLINE=99054745; PubMed=9832547;
RA David D., Sundarababu S., Gerst J.E.;
RT "Involvement of long chain fatty acid elongation in the trafficking of
RT secretory vesicles in yeast.";
RL J. Cell Biol. 143:1167-1182(1998).
RN [6]
RN CHARACTERIZATION.
RX MEDLINE=97362220; PubMed=9211877;
RA Oh C.-S., Toke D.A., Mandala S., Martin C.E.;
RT "ELO2 and ELO3, homologues of the Saccharomyces cerevisiae ELO1 gene,
RT function in fatty acid elongation and are required for sphingolipid
RT formation.";
RL J. Biol. Chem. 272:17376-17384(1997).
CC -!- FUNCTION: Affects plasma membrane H(+)-ATPase activity. May act on a
CC glucose-signaling pathway that controls the expression of several
CC genes that are transcriptionally regulated by glucose such as
CC PMAL1, HXT3 and SNF3. Could be also a component of the membrane
CC bound fatty acid elongation systems that produce the 26-carbon
CC very long chain fatty acids that are precursors for ceramide and
CC sphingolipids. Is essential for the conversion of 24-carbon fatty
CC acids to 26 carbon species.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- SIMILARITY: Belongs to the ELO family.
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CC -----
DR EMBL; L28723; AAA35134.1; -
DR EMBL; X82033; CAAS7553.1; -
DR EMBL; X78326; CAAS5129.1; -
DR EMBL; U19103; AAB67563.1; -
DR EMBL; AF011409; AAC28398.1; -
DR PIR; S48517; S48517.
DR GERMOnline; 142436; -
DR SGD; S0004364; SUR4
DR GO; GO:0005783; C:cytoplasmic reticulum; IDA.
DR GO; GO:0009922; P:fatty acid elongase activity; IMP.
DR GO; GO:0030497; P:fatty acid elongation; IMP.
DR GO; GO:0006892; P:post-Golgi transport; IGI.
DR GO; GO:0030148; P:sphingolipid biosynthesis; IMP.
DR InterPro; IPR002076; GNS1_SUR4.
DR Pfam; PF01151; ELO; 1.
DR PROSITE; PS01188; ELO; 1.

KW Fatty acid biosynthesis; Transmembrane.
PT TRANSMEM 74 94 POTENTIAL.
FT TRANSMEM 106 126 POTENTIAL.
FT TRANSMEM 208 228 POTENTIAL.
FT TRANSMEM 243 263 POTENTIAL.
FT TRANSMEM 284 304 POTENTIAL.
FT CONFLICT 35 35 E -> D (IN REF. 3).
FT CONFLICT 208 208 W -> R (IN REF. 3).
FT CONFLICT 330 331 ST -> FY (IN REF. 3).
SQ SEQUENCE 345 AA; 39465 MW; 1303ASACS4BFCCS CRC64;

Query Match 17.0%; Score 262; DB 1; Length 345;
Best Local Similarity 28.9%; Pred. No. 1.12e-14;
Matches 82; Conservative 53; Mismatches 115; Indels 34; Gaps 11;

QY 27 YKSYHFCEQVADQYWTILFQKQWYHSITSLVLYILKVIQKME--NEKPFLLKYP 84
DB 50 FYFSGYFAEQFEFHINKTEFLAN--GYHVSIIIVYIIIFGQAILRLNASPLKFL 107
QY 85 LILWNGALAAFSIIATLRFSDPLSLYAEQFYKTLG--YSCNPTDVAAFWSFAPALSKI 142
DB 108 FEIHNLFSTISLVLLMLLEQLVPMVYHNGLFWSICKEAFAPKLVTLY--YLYNLTKE 165
QY 143 VELGDTMFIILKRLPLILHYHH--AAVLIVTSGAEHTAAGRFYILMNYFAHSLMYT 200
DB 166 VELIDTVFLVLRKKLLFLHTYHNGATALLCYQLIG--RTSVENVVILLNLGVHVTW 223
QY 201 YTVSGAMGYRFPKVMVMTVTVTQTTMLAGVITWMVYKVKTEY-----KLPQC 249
DB 224 YVFLSSCGIRV--WVKQWTRFQIIQFL--IDLVFVYFATYFYAHKYLDGILPNKGT 279
QY 250 QSVANLYLAFVYVTFPAILTQFPFKAYIIKSSKK--SKSVKNE 291
DB 280 GTQAAAYGYLILFTSYLLLFISFYQSY-----KXGKKTVKKE 318

RESULT 7
ELO4 MACFA STANDARD; PRT; 314 AA.
ID ELO4 MACFA
AC Q95K73;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Elongation of very long chain fatty acids 4 protein.
GN ELOVL4
OS Eukarya, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]_TaxID=9541;
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX MEDLINE=22651945; PubMed=12806887;
RA Umeda S., Ayyagari R., Suzuki M.T., Ono F., Iwata F., Fujiki K.,
RA Kanai A., Takada Y., Yoshikawa Y., Tanaka Y., Iwata T.;
RT "Molecular cloning of ELOVL4 gene from cynomolgus monkey (Macaca
RT fascicularis).";
RL Exp. Anim. 52:129-135(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Temporal cortex;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in the biosynthesis of very long chain fatty
CC acids. Seems to represent a photoreceptor-specific component of
CC the fatty acid elongation system residing on the endoplasmic
CC reticulum.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum (Potential).
CC -!- TISSUE SPECIFICITY: Expressed mainly in retina. Also expressed in

CC skin and thymus.
CC -1- SIMILARITY: Belongs to the ELO family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF4611182; AAO15594.1; -
CC EMBL: AF4611187; AAO15601.1; -
CC EMBL: AF4611183; AAO15601.1; JOINED.
CC EMBL: AF4611184; AAO15601.1; JOINED.
CC EMBL: AF4611185; AAO15601.1; JOINED.
CC EMBL: AF4611186; AAO15601.1; JOINED.
CC EMBL: AB063100; BAB60806.1; -
CC InterPro: IPR002076; GNS1_SUR4.
CC Pfam: PF01151; ELO; 1.
CC PROSITE: PS01188; ELO; 1.
KW Fatty acid biosynthesis; Transmembrane; Endoplasmic reticulum.
FT TRANSMEM 42 62 POTENTIAL.
FT TRANSMEM 78 98 POTENTIAL.
FT TRANSMEM 165 185 POTENTIAL.
FT TRANSMEM 188 208 POTENTIAL.
FT TRANSMEM 247 267 POTENTIAL.
FT SITE 310 312 ENDOPLASMIC RETICULUM RETRIEVAL MOTIF
FT (POTENTIAL).
FT CARBOHYD 20 20 N-LINKED (GLCNAC...) (POTENTIAL).
FT SEQUENCE 314 AA; 36812 MW; 560PE00C91D96766 CRC64;
Query Match 16.9%; Score 261; DB 1; Length 314;
Best Local Similarity 30.3%; Pred. No. 1.3e-14;
Matches 87; Conservative 57; Mismatches 97; Indels 46; Gaps 19;
Qy 22 DMTKYKSYHFFGEQVADQYWTILPKQYHYSITISVLVFLIKVIOKFMENRKEFTL 81
Db 21 DTVEFYRTWSIADKRV---ENNP-LMQSPW---FTLSITLILFLVFMGPKMKMDREPFQM 75
Qy 82 KYPLILWNGALAPSIIATLRFSDPLRSYAEQF---YKTLG---YSCNPTDV---A 130
Db 76 RLVLIIYN-----FGV-LNFFI--FRELFGSYNAGSYVICOVDVSNVNEVRIAA 127
Qy 131 AFSFAPALSKIVELGDMTFILKR--PLIFLHYTHAAVLIVTV-HSGAHTAQR-- 185
Db 128 LMYF---VSKGVEYLDTPFLLAKQNVSLFHVHCT--MFTLWIGIKWVAGQAF 182
Qy 186 FYILMNYFAHSLMYTYTVSAMGYRLPK--WVSMVTVTVOOTMAGVIGITWVYKVKTE 243
Db 183 FGAQNSFIHVMYSYGLAAGFPWIOKYLWKKYLTMLQLVQPHVTHGT--ALSLYTD 240
Qy 244 YKLPQOOSVANLYLAFVIY-VTFALFTQPFVKAYIIKSKKSXVK 289
Db 241 CPFP-----KWHWALIAYSIFLFLNFVIRTY--KEPKKPTGK 280
RESULT 8
ELO4 HUMAN
ID ELO4 HUMAN STANDARD; PRT; 314 AA.
AC Q9GZRS; Q86YJ1; Q9H139;
DT 28-FEB-2003 [rel. 41, Created]
DT 28-FEB-2003 [rel. 41, Last sequence update]
DT 10-OCT-2003 [rel. 42, Last annotation update]
DE Elongation of very long chain fatty acids protein 4.
GN ELOVL4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT VAL-299.
RC TISSUE=Retina;

RX MEDLINE=20578755; PubMed=11138005;
RA Zhang K., Kniazeva M., Han M., Li W., Yu Z., Yang Z., Li Y.,
RA Metzger M.B., Allikmets R., Zack D.J., Kakuk L.E., Jagali P.S.,
RA Wong P.W., McDonald I.M., Sieving P.A., Figueroa D.J., Austin C.P.,
RA Gould R.J., Ayyagari R., Petrukhin K.;
RT "A 5-bp deletion in ELOVL4 is associated with two related forms of
RT autosomal dominant macular dystrophy.";
RL Nat. Genet. 27:89-93 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21464738; PubMed=11581213;
RA Edwards A.O., Donoso L.A., Ritter R. III;
RT "A novel gene for autosomal dominant Stargardt-like macular dystrophy
RT with homology to the SUR4 protein family.";
RL Invest. Ophthalmol. Vis. Sci. 42:2652-2663 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
RA Masuho Y., Nagai K., Isogai T.;
RT "NED0 human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22389257; PubMed=12477932;
RA Klausner R.L., Fellings F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zerbe B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards D.K., Murny D.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Prange C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [5]
RP SEQUENCE OF 35-314 FROM N.A.
RA Dunn M.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP VARIANTS THR-267 AND VAL-299.
RX MEDLINE=22480060; PubMed=12592226;
RA Rivoita C., Ayyagari R., Sieving P.A., Berson E.L., Dryja T.P.;
RT "Evaluation of the ELOVL4 gene in patients with autosomal recessive
RT retinitis pigmentosa and Leber congenital amaurosis.";
RL Mol. Vision 9:49-51 (2003).
CC -1- FUNCTION: Involved in the biosynthesis of very long chain fatty
CC acids. Seems to represent a photoreceptor-specific component of
CC the fatty acid elongation system residing on the endoplasmic
CC reticulum. May be implicated in docosahexaenoic acid (DHA)
CC biosynthesis, which requires dietary consumption of the essential
CC alpha-linolenic acid and a subsequent series of three elongation
CC steps. May be involved in one of these three elongation steps.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum (potential).
CC -1- TISSUE SPECIFICITY: Expressed in the retina and at much lower

level in the brain.

-!- DISEASE: Defects in ELOVL4 are the cause of Stargardt disease 3 (STGD3) [MIM:600110]. STGD3 is an autosomal dominant form of macular degeneration characterized by decreased visual acuity, macular atrophy, and extensive fundus flecks.

-!- DISEASE: Defects in ELOVL4 are a cause of autosomal dominant Stargardt-like macular dystrophy (ADMD) [MIM:600110].

-!- SIMILARITY: Belongs to the ELO family.

-!- DATABASE: NAME=Mutations of the ELOVL4 gene; NOTE=Retina International's Scientific Newsletter; WWW=http://www.retina-international.com/sci-news/elovlmut.htm.

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DR EMBL; AF279654; AAG47669.1; .

DR EMBL; AF279649; AAG47669.1; JOINED.

DR EMBL; AF279650; AAG47669.1; JOINED.

DR EMBL; AF279651; AAG47669.1; JOINED.

DR EMBL; AF279652; AAG47669.1; JOINED.

DR EMBL; AF279653; AAG47669.1; JOINED.

DR EMBL; AF277094; AAG47668.1; .

DR EMBL; AY037298; AAK86839.1; .

DR EMBL; AK055277; BAB70895.1; .

DR EMBL; BC038506; AAR38506.1; .

DR EMBL; AL132875; CAC19496.1; .

DR Genew; HGNC:14415; ELOVL4.

DR MIM; 605512; .

DR MIM; 600110; .

DR GO; GO:0008020; P:G-protein coupled photoreceptor activity; NAS.

DR GO; GO:0006633; P:fatty acid biosynthesis; NAS.

DR InterPro; IPR02076; GNS1_SUR4.

DR Pfam; PF01151; ELO; 1.

DR PROSITE; PS01188; ELO; 1.

XM Fatty acid biosynthesis; Transmembrane; Endoplasmic reticulum;

XM Polymorphism; Stargardt disease; Vision.

FT TRANSMEM 42 62 POTENTIAL.

FT TRANSMEM 78 98 POTENTIAL.

FT TRANSMEM 165 185 POTENTIAL.

FT TRANSMEM 188 208 POTENTIAL.

FT TRANSMEM 247 267 POTENTIAL.

FT SITE 310 312 ENDOPLASMIC RETICULUM RETRIEVAL MOTIF (POTENTIAL).

FT CARBOHYD 20 20 N-LINKED (GLCNAC...) (POTENTIAL).

FT VARIANT 267 267 I -> T.

FT VARIANT 299 299 M -> V.

FT CONFLICT 44 44 /FTID=VAR_012492.

FT SEQUENCE 314 AA; 36829 MW; B2BCE54D868E96E CRC64;

Query Match 16.4%; Score 254; DB 1; Length 314;

Best Local Similarity 27.5%; Pred. No. 4.8e-14;

Matches 79; Conservative

QY 22 DMTTKYKYSHPGEGQVADQVYTLFQKYVHSITISLVYFLIKVIOKVENRKPFTL 81

DB 21 DTVEFYRWTSIADKRV---ENWP-LMQSPW-PTLSISTLYLLFWLWGPWKMKDRPFQM 75

QY 82 KYPLILNGLAALAFSIIATLRFSDPLRSYABGFKYTKLCYSCNPTD-----VA 130

DB 76 RLVLIIYFNGVLLNLEFI-----PREFLMSYAGSYICQSDVSNVHEVRIAA 127

QY 131 AFWSFAPALSKIVELGDTMFIILKR--PLIFLHYTHAAVLITYV-HSGAEHTAGR-- 185

DB 128 LMYF---VSKGVEYLDVTFEILKKNQVSLFVYHCT--NFTLWIGIKWVAGGQAF 182

QY 186 FYLLMNYFAHSLMYTYTTSVAMGYRLPK--WVSMVTVTVTQTLQAGVIGTWVYVKVTE 243

DB 183 FQAQLNSIHVMYSYGLTAFGPMIQKYLWKRVLTLQLIQFHTTIGHT--ALSLYTD 240

QY 244 YKLPCQSQSWANLYLAFVY-VTFALFTQFFKAVYIIKSSKKSXKSVK 289

DB 241 CPFP-----KMHWALIAVAISFIFLFLNFVIRTY--KEPKPKAGK 280

RESULT 9

ELO1 MOUSE

AC Q9JLJ5; Q9D1B2; STANDARD; PRT; 279 AA.

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Elongation of very long chain fatty acids protein 1.

GN ELOVL1 OR SSCI.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RC SEQUENCE FROM N.A.

RP STRAIN=BALB/c; TISSUE=Liver;

RX MEDLINE=20253178; PubMed=10791983;

RA Tordik P., Westerberg R., Silve S., Asadi A., Jakobsson A., Cannon B., Loison G., Jacobsson A.,

RA "Role of a new mammalian gene family in the biosynthesis of very long chain fatty acids and sphingolipids.";

RT J. Cell Biol. 149:707-718(2000).

RN [2]

RC SEQUENCE FROM N.A.

RP TISSUE=Breast tumor;

RX MEDLINE=22388257; PubMed=12477932;

RA Klausner R.B., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buotow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., McKernan K.J., Malek J.A., Qunaratne P.H.,

RA Bosak S.A., McEwan P.J., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards D., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [3]

RC SEQUENCE OF 78-279 FROM N.A.

RP STRAIN=C57BL/6J; TISSUE=Embryo;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawal J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo J., Yamanaka I.,

RA Saio T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saio R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.N., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbearts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).
CC -!- FUNCTION: Could be implicated in tissue-specific synthesis of very
CC long chain fatty acids and sphingolipids. May catalyze one or both
CC of the reduction reaction in fatty acid elongation, i.e.,
CC conversion of beta-ketoacyl CoA to beta-hydroxyacyl CoA or
CC reduction of trans-2-enoyl CoA to the saturated acyl CoA
CC derivative.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum (potential).
CC -!- TISSUE SPECIFICITY: Expressed in a broad variety of tissues.
CC Highly expressed in stomach, lung, kidney, skin and intestine.
CC Moderately expressed in white adipose tissue, liver, spleen,
CC brain, brown adipose tissue, heart and muscle. Weakly expressed in
CC testis.
CC -!- SIMILARITY: Belongs to the ELO family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF170907; AAF72572.1; -;
CC EMBL; BC006735; AAH06735.1; -;
CC EMBL; AK003743; BAB22975.1; -;
CC MGD; MGI:1858959; Elov11.
CC InterPro; IPR002076; GNS1_SUR4.
CC Pfam; PF0151; ELO; 1.
CC PROSITE; PS01188; ELO; 1.
CC Fatty acid biosynthesis; Transmembrane; Endoplasmic reticulum.
CC POTENTIAL.
CC TRANSMEM 23 43
CC TRANSMEM 61 81
CC TRANSMEM 176 196
CC TRANSMEM 203 223
CC TRANSMEM 231 251
CC SITE 275 277
CC
CC CONFLICT 78 79 YE -> MR (IN REF. 3).
CC SEQUENCE 279 AA; 32678 MW; CASAI0CF55FDB2F76 CRC64;
CC
CC Query Match 15.5%; Score 239.5; DB 1; Length 279;
CC Best Local Similarity 28.6%; Pred. No. 6.8e-13;
CC Matches 78; Conservative 51; Mismatches 101; Indels 43; Gaps 13;
CC
CC QY 39 ADP--QYWTILPQKYWHSITISVLYFILIKVIQFMENRKPFTLYPLILWNGALAAFS 96
CC
CC Db 15 ADPRIQSVPLMGSPLLITSLITLVYVFFIL-SIGPRIMANRPFQLRGFMVYVNSLVLS 73
CC
CC QY 97 ITATURFSDIPRSYAGFYKTYLCYCNPTD-----VAAPWFAFALSIVELG 146
CC
CC Db 74 LVIYVEFLM-----SGWLSTYTWRCDDPDSNSPEALRMVRVAV--LPLMSKVIELM 123
CC
CC QY 147 DTMPILRKES--PLIFLYVYHAAVLIVYHSGAHT--AAGRFFYLMNYFAHSLMYTYY 202
CC
CC Db 124 DIVIFILRKQOQVTFLLVHFH-SVLPWSWVWGIKIAQGWGSGFAMINSSVHVYVLYY 182
CC
CC QY 203 TVSANGYRLP-----KWSMTVTVYVQTQ-MIAGVITVMYKVTYKLPQQQSVANLY 256
CC
CC Db 183 GLSALG--PVAQPVLMKKHMTAQILQFVLVLSLHISQYFMPSCNYQP-----IIIH 234
CC
CC QY 257 LAFVIYVTFAILFIQFVKAVIKKSKSKSVK 289
CC
CC Db 235 LIWYGTIFPLFSFWHSY-TKGRLPRAVO 266

RESULT 10
ELO1_HUMAN

ID ELO1_HUMAN STANDARD; PRT; 279 AA.
AC Q9BWM0; Q9NVD9; Q9Y396;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Elongation of very long chain fatty acids protein 1 (CGI-88).
GN ELOVLI OR SSC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20272150; PubMed=10810093;
RA Lai C.-H., Chou C.-Y., Chang L.-Y., Lin C.-S., Lin W.-C.;
RT "Identification of novel human genes evolutionarily conserved in
RT Caenorhabditis elegans by comparative proteomics.";
RL Genome Res. 10:703-713(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
RA Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
RA Nakamura Y., Nagahari K., Masuko Y., Sasaki N.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max J., Wang J., Haie H.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.B., Scheetz T.B.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Wozney K.D., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield V.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Could be implicated in tissue-specific synthesis of very
CC long chain fatty acids and sphingolipids. May catalyze one or both
CC of the reduction reaction in fatty acid elongation, i.e.,
CC conversion of beta-ketoacyl CoA to beta-hydroxyacyl CoA or
CC reduction of trans-2-enoyl CoA to the saturated acyl CoA
CC derivative (by similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum (potential).
CC -!- SIMILARITY: Belongs to the ELO family.
CC -!- CAUTION: Ref.1 sequence differs from that shown due to a
CC frameshift in position 189.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF151846; AAD34083.1; ALT_FRAME.
CC EMBL; AK001653; BAA91813.1; -;
CC EMBL; BC000618; AAH00618.1; -;

QY 144 ELGDTMFIILRKRLI-----FLHY-----YHRAVLI 171
Db 154 -IGSLIAALLISLATAAFAYMFAFRVKSLEEFKEIFPGSGEMHFSALLPASFLISAALI 212
QY 172 Y-----TVHSGAEH-TARGFVILNNYFAHSLMYTIVTSAMGYRLPKWVSMTVTVTQFT 225
Db 213 YLSRFEIVHS--EHGLISGASVDVNILSPSLMF-----LSAI 248
QY 226 QMLAGVGIITMVKYKTEYKLPQOSVANLYLAFVIYVTFAILFOFFKAYIIKSKKS 285
Db 249 VLLSGIIFAAYIVARRRVERVF---QIVGVFLVIALLLTFV---APFFVQKFEVVEPSLS 301

Search completed: June 16, 2004, 15:28:01
Job time : 18 secs

Db 260 KPMKDMQEPAGKEVKN 277
RESULT 15
ID YE21_ARCFU STANDARD; PRT; 880 AA.
AC O28851;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Hypothetical UPF0182 protein AF1421.
GN AF1421.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
3N
2P SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-P., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Winn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Graham D.E., Kyripides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Sadger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Uterback T.,
RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the UPF0182 family.

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EXEL; AE001005; AAB89825.1; --
DR FIR; D69427; D69427.
DR TIGR; AF1421; --
DR HAKAP; MF_01600; -- 1.
DR InterPro; IPR005372; UPF0182.
DR Pfam; PF03699; UPF0182; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 19 41 POTENTIAL.
FT TRANSMEM 61 83 POTENTIAL.
FT TRANSMEM 103 125 POTENTIAL.
FT TRANSMEM 152 174 POTENTIAL.
FT TRANSMEM 195 217 POTENTIAL.
FT TRANSMEM 237 259 POTENTIAL.
FT TRANSMEM 268 290 POTENTIAL.
SQ SEQUENCE 880 AA; 102210 MW; 8AD99AB7B4E50671 CRC64;

Query Match 6.6%; Score 102; DB 1; Length 880;
Best Local Similarity 19.3%; Pred. No. 0.58;
Matches 58; Conservative 47; Mismatches 83; Indels 112; Gaps 13;

QY 47 LFKYWHISITISVLYFILIYQKFMENRKPFTLKPLILWNGALAAFSIATIRFSID 106
Db 53 VFLTYLKHSLGFFPLEFIIFV-----PLFLTNVAVRK-----VLEFHGE 93
QY 107 PIR-----SLYAGFYKYLCSNPDTV-----AATWSFAFALSKIV 143
Db 94 PLKIHPLADFGIAPTAALTAVNNWSSMLFYFNSSNFGVSDPIFGIDRAFYTFQPLFKIV 153

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2004, 15:21:03 ; Search time 60 Seconds
(without alignments)
1370.355 Million cell updates/sec

Title: US-09-936-845a-15

Perfect score: 1545
Sequence: 1 MELAEFWNDLNTFTTYGNH.....FFVKAYIKSKKSKSVKNE 291

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1545	100.0	291	3 AAB00198	Aab00198 Putative
2	564	36.5	435	3 AAB00199	Aab00199 Putative
3	547	35.4	269	3 AAB00205	Aab00205 Putative
4	492	31.8	270	4 AAE04173	Aae04173 Human gen
5	492	31.8	270	5 ABG92079	Abg92079 Human xec
6	492	31.8	270	5 AAE24550	Aae24550 Human ELG
7	492	31.8	270	5 ABB78813	Abb78813 Human NOV
8	492	31.8	270	5 ABB78812	Abb78812 Human NOV
9	492	31.8	270	5 ABP56418	Abp56418 Human LCE
10	492	31.8	270	5 ABB82960	Abb82960 Human LCE
11	492	31.8	270	6 ABB82966	Abb82966 Human LCE
12	485.5	31.4	278	3 AAY79263	Aay79263 Putative
13	485.5	31.4	278	5 AAU87829	Aau87829 Fruitfly
14	484.5	31.4	313	4 ABB60310	Abb60310 Drosophila
15	483.5	31.3	263	6 AAE37330	Aae37330 Human VLC
16	483	31.3	270	4 AAE04172	Aae04172 Human gen
17	479	31.0	271	3 AAY79260	Aay79260 Putative
18	479	31.0	271	4 ABA48959	Ab48959 Mouse fat
19	479	31.0	271	5 ABP56420	Abp56420 Human elo
20	479	31.0	272	3 AAY79249	Aay79249 Human put
21	478	30.9	271	3 AAB00209	Aab00209 Murine se
22	476.5	30.8	261	3 AAY79264	Aay79264 Putative
23	469	30.4	236	5 ABP56419	Abp56419 Human elo
24	469	30.4	236	6 ABB82959	Abb82959 Human LCE
25	451	29.2	269	5 ABB78814	Abb78814 GNS1/SUR4

26	437.5	28.3	265	5	AAE24555	Aae24555 Human ELG
27	435.5	28.2	265	3	AAAY79266	Aay79266 Human elo
28	435.5	28.2	265	3	AAAB29648	Aab29648 Human mem
29	435.5	28.2	265	4	AAU000476	Aau000476 Human INT
30	435.5	28.2	265	5	AAU87832	Aau87832 Human elo
31	435.5	28.2	265	5	AAU87832	Aau87832 Human elo
32	435.5	28.2	265	6	AAU879838	Aau879838 ADSL rela
33	435.5	28.2	265	6	ABO32607	Ab032607 Secreted
34	435.5	28.2	265	6	ABO32621	Ab032621 Secreted
35	435.5	28.2	265	6	ABB82962	Abb82962 Human LCE
36	435.5	28.2	265	6	ABB82961	Abb82961 Human LCE
37	434.5	28.1	240	4	ABO07183	Ab007183 Human p53
38	433	28.0	216	4	AAU93344	Aau93344 Human pol
39	433	28.0	216	5	AAE04100	Aae04100 Human gen
40	424	27.4	216	4	AAE04123	Aae04123 Human alb
41	424	27.4	216	5	ABG64365	Abg64365 Human alb
42	413.5	26.8	219	6	ABO32609	Ab032609 Secreted
43	398	25.8	274	3	AAAB00200	Aab00200 Putative
44	374	24.2	274	3	AAAB00202	Aab00202 Putative
45	370.5	24.0	297	4	AAAB86466	Aab86466 Thraustoc

ALIGNMENTS

RESULT 1
AAB00198
ID AAB00198 standard; protein; 291 AA.

XX
AC AAB00198;
XX
DT 08-FEB-2001 (first entry)
XX
DE Putative polyunsaturated fatty acid elongase (PUFA).
XX
KW Elongase; polyunsaturated fatty acid; PUFA; dietary supplement;
KW pharmaceutical; foodstuff; food; di-homo-gamma-linoleic acid;
KW arachidonic acid; eicosapentaenoic acid; docosatrienoic acid;
KW docosatetraenoic acid; docosapentaenoic acid; docosahexaenoic acid.
XX
OS Caenorhabditis elegans.
XX
PN WO200005330-A1.
XX
PD 21-SEP-2000.
XX
PF 20-MAR-2000; 2000WO-GB001035.
XX
PR 18-MAR-1999; 99GB-00006307.
XX
PR 18-FEB-2000; 2000GB-00003869.
XX
PA (UYBR-) UNIV BRISTOL.
XX
PI Napier JA;
XX
DR WPI; 2000-647074/62.
XX
PT Novel isolated polypeptide comprising functional long chain
PT polyunsaturated fatty acid (PUFA) elongase of Caenorhabditis elegans used
PT to produce PUFA for foodstuff, dietary supplement or pharmaceutical
PT composition.
XX
PS Disclosure; Page 25; 42pp; English.

XX
CC New elongase polypeptides which are functional long chain polyunsaturated
CC fatty acid (PUFA) elongase polypeptides are described. The elongase
CC catalyses an elongase reaction to produce PUFA (a 24 carbon fatty acid
CC with at least 4 double bonds) such as di-homo-gamma-linoleic acid
CC (20:3Delta5,11,14), arachidonic acid (20:4Delta5,8,11,14),
CC eicosapentaenoic acid (20:5Delta5,8,11,14,17), docosatrienoic acid
CC (22:3Delta3,15,19), docosatetraenoic acid (22:4Delta7,10,13,16),
CC docosapentaenoic acid (22:5Delta7,10,13,16,19) or docosahexaenoic acid
CC (22:6Delta7,10,13,16,19). PUFA produced is useful in foodstuffs,

CC dietary supplements and in pharmaceutical compositions which can then be
 CC used to elavate PUFA levels of an animal or plant
 XX
 SQ Sequence 291 AA;

Query Match 100.0%; Score 1545; DB 3; Length 291;
 Best Local Similarity 100.0%; Pred. No. 2.7e-161;
 Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELAEFNDLNTFIYGNHTDMTKYKSYHPPGEQVADPOYWTILFQKYWHYSITISV 60
 DB 1 MELAEFNDLNTFIYGNHTDMTKYKSYHPPGEQVADPOYWTILFQKYWHYSITISV 60

QY 61 LYFLIKVIOKFMENRPFLLKYLPLILWNGALAAFSIIATLRSIDPLRSYAEQFYKTL 120
 DB 61 LYFLIKVIOKFMENRPFLLKYLPLILWNGALAAFSIIATLRSIDPLRSYAEQFYKTL 120

QY 121 CYSNPTDVAAPWSFAPALSKIVELGDTMFIILKRPLILFLYHHAAVLIIYVHSGAEH 180
 DB 121 CYSNPTDVAAPWSFAPALSKIVELGDTMFIILKRPLILFLYHHAAVLIIYVHSGAEH 180

QY 181 TAAGRFILMNYFAHSLMYTYVTSAMGYRLPKWVSMVTVTVOFTQMLAGVGIWMVYKV 240
 DB 181 TAAGRFILMNYFAHSLMYTYVTSAMGYRLPKWVSMVTVTVOFTQMLAGVGIWMVYKV 240

QY 241 KTEYKLPQOSVANLYLAFVIYVTFAILFIQFFVKAVIIKSSKSKSVKNE 291
 DB 241 KTEYKLPQOSVANLYLAFVIYVTFAILFIQFFVKAVIIKSSKSKSVKNE 291

RESULT 2
 AAB00199
 ID AAB00199 standard; protein; 435 AA.
 XX
 AC AAB00199;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Putative polynunsaturate fatty acid elongase (PUFA).
 XX
 KW Elongase; polyunsaturated fatty acid; PUFA; dietary supplement;
 KW pharmaceutical; foodstuff; food; di-homo-gamma-linoleic acid;
 KW arachidonic acid; eicosapentaenoic acid; docosatrienoic acid;
 KW docosatetraenoic acid; docosapentaenoic acid; docosahexaenoic acid.
 XX
 OS Caenorhabditis elegans.
 XX
 PN WO200055330-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 20-MAR-2000; 2000WO-GB001035.
 XX
 PR 18-MAR-1999; 99GB-00006307.
 PR 18-FEB-2000; 2000GB-00003869.
 XX
 PA (UYBR-) UNIV BRISTOL.
 XX
 PI Napier JA;
 XX
 DR WPI; 2000-647074/62.
 XX
 PT Novel isolated polypeptide comprising functional long chain
 PT polyunsaturated fatty acid (PUFA) elongase of Caenorhabditis elegans used
 PT to produce PUFA for foodstuff, dietary supplement or pharmaceutical
 PT composition.
 XX
 PS Disclosure; Page 25-26; 42pp; English.
 XX
 CC New elongase polypeptides which are functional long chain polyunsaturated
 CC fatty acid (PUFA) elongase polypeptides are described. The elongase
 CC catalyses an elongase reaction to produce PUFA (a 24 carbon fatty acid
 CC with at least 4 double bonds) such as di-homo-gamma-linoleic acid

CC (20:3Delta8,11,14), arachidonic acid (20:4Delta5,8,11,14),
 CC eicosapentaenoic acid (20:5Delta5,8,11,14,17), docosatrienoic acid
 CC (22:3Delta3,15,19), docosatetraenoic acid (22:4Delta7,10,13,16),
 CC docosapentaenoic acid (22:5Delta7,10,13,16,19) or docosahexaenoic acid
 CC (22:6Delta7,10,13,16,19). PUFA produced is useful in foodstuffs,
 CC dietary supplements and in pharmaceutical compositions which can then be
 CC used to elavate PUFA levels of an animal or plant
 XX
 SQ Sequence 435 AA;

Query Match 36.5%; Score 564; DB 3; Length 435;
 Best Local Similarity 42.0%; Pred. No. 4.4e-53;
 Matches 128; Conservative 45; Mismatches 86; Indels 46; Gaps 7;

QY 22 DMTKY---KSYHPPGEQVADPOYWTILFQKYWHYSITISVLYFILI---KVI----- 69
 DB 5 DYNPKYGLNYSIFLPPFETSPDAFRSTTWQNHWTQSITASVVVAVIFGKKVLIYKK 64

QY 70 -----QKQ---MENRKPFTLKYLPLILWNGALAAFSIIATLR 102
 DB 65 SRVITFESSLQNAIKNRNKSINSSQFQIMKYPQLDTPLFWNSFLAIFSLGLFLR 124

QY 103 FSDIDPLRSLYAEG--PYKTLCYSCNPTDVAAPWSFAPALSKIVELGDTMFIILKRPLIP 160
 DB 125 MTEPFVWSKSAEGNSFKYSICHSSYAQGVTFWTEQFAMSKLPELIDTIFIVLRKPLIP 184

QY 161 LHYTHPAVLIIYVHSGAEHTAAGRFILMNYFAHSLMYTYVTSAMGYRLPKWVSMVT 220
 DB 185 LHWYHVTVMYTHAYKDHDTASGRFIMWYGVHMYALSYVALSKLRLPKQMANVVT 244

QY 221 TVOTQMLAGVGIWMVYKVKT--EYKLPQOSVANLYLAFVIYVTFAILFIQFFVKAVI 278
 DB 245 TLQALQVWGVIIIVTVYIKSSGEY---CQQTWDNLGICFGVYFTYFLLFANFFYHAVV 301

QY 279 IKSSK 283
 DB 302 KKNR 306

RESULT 3
 AAB00205
 ID AAB00205 standard; protein; 269 AA.
 XX
 AC AAB00205;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Putative polynunsaturate fatty acid elongase (PUFA).
 XX
 KW Elongase; polyunsaturated fatty acid; PUFA; dietary supplement;
 KW pharmaceutical; foodstuff; food; di-homo-gamma-linoleic acid;
 KW arachidonic acid; eicosapentaenoic acid; docosatrienoic acid;
 KW docosatetraenoic acid; docosapentaenoic acid; docosahexaenoic acid.
 XX
 OS Caenorhabditis elegans.
 XX
 PN WO200055330-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 20-MAR-2000; 2000WO-GB001035.
 XX
 PR 18-MAR-1999; 99GB-00006307.
 PR

QY 227 MLAGVGITWVYKTEYKLPQOOSVANLYAFVIVTFAILFIQFPVAYI---IKSSK 283
DB 210 MFGAIVSILTYIWRQDQ--GCHTMEHLFWSLTYWYFILFAHPCQTYIRPKVAKT 267
QY 284 KSK 286
DB 268 KSQ 270

RESULT 5
ID ABG92079 standard; protein; 270 AA.
AC ABG92079;
XX
DT 29-NOV-2002 (first entry)
XX
DE Human receptors and membrane associated protein REMAP-22.
XX
XX Human; receptor and membrane-associated protein; REMAP; atherosclerosis;
XX cardiovascular disorder; hypertension; congestive heart failure; oedema;
XX aneurysm; angina pectoris; ischaemic heart disease; lung disease; nausea;
XX rheumatic heart disease; chronic obstructive pulmonary disease; anaemia;
XX emphysema; bronchitis; gastrointestinal disorder; peptic ulcer; asthma;
XX Crohn's disease; lipid metabolism disorder; Fabry's disease; dementia;
XX pancreatitis; diabetes mellitus; hyperlipidaemia; autoimmune disorder;
XX inflammatory disorder; neurological disorder; Creutzfeldt-Jakob disease;
XX cell proliferative disorder; protein replacement therapy; adenocarcinoma;
XX developmental disorder; metabolic disorder; Alzheimer's disease; stroke;
XX Parkinson's disease; multiple sclerosis; Cushing's syndrome; anxiety;
XX schizophrenia; Addison's disease; endocrine disorder; gene therapy; gout;
XX amnesia; cancer; leukaemia; lymphoma; myeloma; sarcoma.
XX
XX Homo sapiens.
XX
XX WO200263006-A2.
XX
XX 15-AUG-2002.
XX
XX 05-FEB-2002; 2002WO-US0039868.
XX
XX 06-FEB-2001; 2001US-0267201P.
XX 16-FEB-2001; 2001US-0269580P.
XX 09-APR-2001; 2001US-0282679P.
XX 02-MAY-2001; 2001US-0288293P.
XX 14-JAN-2002; 2002US-0348687P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Azimzai Y, Yue H, Ding L, Nguyen DB, Gandhi AR, Burford N;
XX Thangavelu K, Elliott VS, Ramkumar J, Yao MG, Lal PG, Tang TY;
XX Swarnakar A, Warren BA, Walla NK, Policky JL, Xu Y, Honchell CD;
XX Au-Young J, Baughn MR, Duggan BK, Lu DAM, Gietzen KJ, Hillmann JU;
XX Raumann BE, Lu Y, Sapperstein SK, Tran UK, Richardson TW;
XX Emerling BW, Hafalia AJA, Burriell JD, Marcus GA, Zingler KA;
XX Kable AE, Gorward AE;
XX
XX WPI: 2002-627559/67.
XX N-PSDB; AS67800.
XX
XX New human receptor and membrane-associated proteins and polynucleotides,
XX useful for diagnosing, treating or preventing cardiovascular disorders
XX (e.g. aneurysms), neurological disorders (e.g. Parkinson's disease) or
XX cancers.
XX
XX Claim 2; Page 190-191; 262pp; English.
XX
XX The present invention relates to a new receptor and membrane-associated
XX protein (REMAP). The polypeptide, polynucleotide and agonist are useful
XX for treating a condition associated with decreased expression of
XX functional REMAP. The antagonist is useful for treating a disease
XX associated with overexpression of functional REMAP. The anti-REMAP

CC antibody is useful for diagnosing a condition or disease associated with
CC the expression of REMAP. These polypeptides, polynucleotides, agonists
CC and antagonists are particularly useful for diagnosing, treating or
CC preventing cardiovascular (e.g. atherosclerosis, hypertension, aneurysms,
CC congestive heart failure, angina pectoris, or ischaemic or rheumatic
CC heart disease), lung (e.g. oedema, chronic obstructive pulmonary disease,
CC emphysema or bronchitis) gastrointestinal (e.g. nausea, peptic ulcer or
CC Crohn's disease), lipid metabolism (e.g. Fabry's disease, diabetes
CC mellitus or hyperlipidaemia), autoimmune/inflammatory (e.g. anaemia,
CC asthma, gout, pancreatitis or Crohn's disease), neurological (e.g.
CC dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease,
CC multiple sclerosis, Parkinson's disease, anxiety, schizophrenia or
CC amnesia), metabolic (e.g. Addison's disease), developmental (e.g.
CC Cushing's syndrome), endocrine or cell proliferative disorders (e.g.
CC cancers including adenocarcinoma, leukaemia, lymphoma, myeloma or
CC sarcoma). The present amino acid sequence represents a human REMAP
CC protein of the invention
XX
SQ Sequence 270 AA;
Query Match 31.8%; Score 492; DB 5; Length 270;
Best Local Similarity 39.9%; Pred. No. 2e-45;
Matches 97; Conservative 53; Mismatches 87; Indels 6; Gaps 3;
QY 48 FQKYVYHSITISVLYPILIKVIQKFMENRKPFTLKYPILMNGALAAFSIIATLRFSDP 107
DB 30 FEEVWATSPPIALYLVLAIVGQVYKRGFNQLQGPLILWSFCLAFPSILGAVRWGIM 89
QY 108 IRLSYAEGYKILCY-SCNPTDVAATWSPALSKIVELGDTMFIILKRPILFLHYHH 166
DB 90 GTVLLTGLKQKQFCNFINFINDNSTVKFMSWVFLSKVIELGDTAFIILKRPILFIHWYH 149
QY 167 AAVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYTTSVAMGYRLPKVSMVTVTQTQ 226
DB 150 STVLVTSFGYKKNKVPAGGFVTNFGVHALMYTYTLKAAVKKPKQLPMLTSLILQ 209
QY 227 MLAGVGITWVYKTEYKLPQOOSVANLYAFVIVTFAILFIQFPVAYI---IKSSK 283
DB 210 MFGAIVSILTYIWRQDQ--GCHTMEHLFWSLTYWYFILFAHPCQTYIRPKVAKT 267
QY 284 KSK 286
DB 268 KSQ 270

RESULT 6
AAE24550
ID AAE24550 standard; protein; 270 AA.
XX
XX AAE24550;
XX
XX 04-NOV-2002 (first entry)
XX
XX Human ELG6 protein.
XX
XX Human; elongase; therapy; enzyme; polyunsaturated fatty acid; sinusitis;
XX PUPA disorder; cardiovascular disorder; articular cartilage degradation;
XX peripheral vascular disease; atherosclerosis; coronary artery disease;
XX inflammatory disorder; pancreatitis; asthma; gastrointestinal disorder;
XX osteoarthritis; rheumatoid arthritis; congenital liver disease; cancer;
XX acne; Sjogren's syndrome; body weight disorder; cerebrovascular disease;
XX acute respiratory distress syndrome; hypercholesterolaemia; alcoholism;
XX postviral fatigue; psychiatric disorder; pre-menstrual syndrome; eczema;
XX Alzheimer's syndrome; hypertriglyceridaemia; cystic fibrosis; anorexia;
XX autoimmune disorder; obesity; cachexia; viral disease; endometriosis;
XX dyslipidaemia; atopic disorder; diabetes; ELG6.
XX
XX Homo sapiens.
XX
XX WO200244320-A2.
XX
XX 06-JUN-2002.
XX

QY 48 FOKYVHSHITISVLYFILLIKVIOKEMENKFTLKYPLILWNGALAAFSIIATLRFSDP 107
 DB 103 FRYWATSPFIALIYLVIAVGQNYKBERGFLNQLGPIILWSFCLAFISILGAVRWGIM 89
 QY 108 LRSIYABGEFKTLCY-SCNPTDVAAFWSPAFALSKIVELGDTWTFIILRKPLIFLHYHH 166
 DB 90 GTVLLTGLAQTVCFINFDNNTVKFWSVLLSKVIELGDTAFIILRKPLIFLHYHH 149
 QY 167 AAVLIYVTHSGAEHTAAGRFYILMNYFAHSLMYYTIVTSAMGVRLEPKWMSMTVTQTQ 226
 DB 150 STVLVYTSFGYKXKVPAGGFVTFMFGVHAIMYTYTLKAANKVPPKMLPMLTISQILD 209
 QY 227 MLAGVGITWVYKVKTEYKLPQQSVANLYLAFVIYVTFAILFIQFFVKAYI---IKSSK 283
 DB 210 MFVGAIVSILTYIWRQDQ--GCHTMEHLFWSPILMYTYLFAHFFCQYIIPKVKAKT 267
 QY 284 KSK 286
 DB 268 XSQ 270

RESULT 8
 ABB78812
 ID ABB78812 standard; protein; 270 AA.
 AC ABB78812;
 DT 29-JUL-2002 (first entry)
 DE Human NOV6a protein sequence SEQ ID NO:18.
 KW Human; NOVX; cytostatic; antiarteriosclerotic; cardiovascular; lymphoma;
 KW anti-diabetic; immunosuppressive; neuroprotective; gene therapy; cancer;
 KW cardiomyopathy; atherosclerosis; cell signal processing; diabetes; AIDS;
 KW metabolic pathway modulation; neoplastic; neurological disorder; asthma;
 KW adenocarcinoma; prostate cancer; uterus cancer; immune response;
 KW Crohn's disease; multiple sclerosis; Graft versus host disease;
 KW chromosome 10.
 OS Homo sapiens.
 XX WO200230974-A2.
 XX 18-APR-2002.
 XX 12-OCT-2001; 2001WO-0301922.
 XX 12-OCT-2000; 2000US-0240113P.
 XX 16-OCT-2000; 2000US-0240625P.
 XX 16-OCT-2000; 2000US-0240637P.
 XX 16-OCT-2000; 2000US-0240648P.
 XX 16-OCT-2000; 2000US-0240662P.
 XX 16-OCT-2000; 2000US-0240669P.
 XX 16-OCT-2000; 2000US-0240703P.
 XX 16-OCT-2000; 2000US-0240732P.
 XX 16-OCT-2000; 2000US-0241190P.
 XX 18-JAN-2001; 2001US-0262455P.
 XX (CURA-) CURAGEN CORP.
 XX (MILL/) MILLET I.
 XX Grosse WM, Alsobrook JP, Lepley DM, Burgess CE, Mishra V;
 XX Kekuda R, Li L, Padigaru M, Shimkets RA, Zerhusen BD, Spytek KA;
 XX Edinger S, Gerlach V, Macdougall J, Stone D, Gunther E, Ellerman K;
 XX WPI; 2002-444172/47.
 XX DR N-PSDB; ABN86918.
 XX New NOVX polypeptides and polynucleotides, useful for treating or
 XX preventing a NOVX-associated disorder or a pathological state in a
 XX subject, particularly a human, e.g. cardiomyopathy, atherosclerosis,
 XX cancer or diabetes.

PS Claim 1; Page 52; 227pp; English.
 XX The present invention describes novel human proteins designated NOVX
 CC (where X is 1, 2a, 2b, 2c, 2d, 3, 4, 5, 6a, 6b, 7, 8, or 9). NOV1 is a
 CC tyrosine-protein kinase 6-like protein; NOV2a-d are keratin 4-like
 CC proteins; NOV3 is a collagen-like protein; NOV4 is a cystatin B-like
 CC protein; NOV5 is a serotonin receptor-like protein; NOV6a and NOV6sv are
 CC cold inducible glycoprotein 30-like proteins; NOV7 is a matrilin-2-like
 CC protein; NOV8 is a leukocyte surface antigen (CD53)-like protein; and
 CC NOV9 is a tyrosine kinase-like protein. NOVX sequences have cytostatic,
 CC antiarteriosclerotic, cardiovascular, anti-diabetic, immunosuppressive and
 CC neuroprotective activities, and can be used in gene therapy. The NOVX
 CC sequences can be used in therapeutics, particularly for treating,
 CC preventing or alleviating a NOVX-associated disorder or a pathological
 CC state in a subject, particularly a human. These disorders include
 CC cardiomyopathy, atherosclerosis, a disorder related to cell signal
 CC processing and metabolic pathway modulation or diabetes. The NOVX
 CC sequences are also useful for determining the presence of or
 CC predisposition to a disease associated with altered levels of NOVX
 CC polypeptide or nucleic acid, particularly cancer. The NOVX sequences are
 CC especially useful in therapeutic or prophylactic applications for
 CC neoplastic or neurological disorders, and in the treatment of
 CC adenocarcinoma, lymphoma, prostate cancer, uterus cancer, immune
 CC response, AIDS, asthma, Crohn's disease, multiple sclerosis or Graft
 CC versus host disease. The present sequence represents the human NOV6a
 CC protein from the present invention. NOV6a is located to chromosome 10
 XX Sequence 270 AA;
 SQ Query Match 31.8%; Score 492; DB 5; Length 270;
 Best Local Similarity 39.9%; Pred. No. 2e-45;
 Matches 97; Conservative 53; Mismatches 87; Indels 6; Gaps 3;
 QY 48 FOKYVHSHITISVLYFILLIKVIOKEMENKFTLKYPLILWNGALAAFSIIATLRFSDP 107
 DB 30 FRYWATSPFIALIYLVIAVGQNYKBERGFLNQLGPIILWSFCLAFISILGAVRWGIM 89
 QY 108 LRSIYABGEFKTLCY-SCNPTDVAAFWSPAFALSKIVELGDTWTFIILRKPLIFLHYHH 166
 DB 90 GTVLLTGLAQTVCFINFDNNTVKFWSVLLSKVIELGDTAFIILRKPLIFLHYHH 149
 QY 167 AAVLIYVTHSGAEHTAAGRFYILMNYFAHSLMYYTIVTSAMGVRLEPKWMSMTVTQTQ 226
 DB 150 STVLVYTSFGYKXKVPAGGFVTFMFGVHAIMYTYTLKAANKVPPKMLPMLTISQILD 209
 QY 227 MLAGVGITWVYKVKTEYKLPQQSVANLYLAFVIYVTFAILFIQFFVKAYI---IKSSK 283
 DB 210 MFVGAIVSILTYIWRQDQ--GCHTMEHLFWSPILMYTYLFAHFFCQYIIPKVKAKT 267
 QY 284 KSK 286
 DB 268 XSQ 270

RESULT 9
 ABB56418
 ID ABB56418 standard; protein; 270 AA.
 AC ABB56418;
 XX 12-MAR-2003 (first entry)
 XX Human elongase HSELO1-like protein SEQ ID NO:2.
 KW Human; elongase; elongase HSELO1-like protein; enzyme; cytostatic;
 KW anti-diabetic; antiasthmatic; anti-HIV; antiparkinsonian; neurotropic;
 KW neuroprotective; tranquillisier; antimigraine; analgesic; neuroleptic;
 KW cerebroprotective; gene therapy; cancer; diabetes; CNS disorder; asthma;
 KW metabolic disease; central nervous system disorder; COPD; dementia;
 KW Parkinson's disease; multiple sclerosis; stroke; Alzheimer's disease;
 KW Huntington's disease; Creutzfeldt-Jakob disease; HIV; schizophrenia;
 KW psychosis; attention deficit disorder; headache pain; migraine.

```
OS Homo sapiens.
XX WO200262974-A2.
XX 15-AUG-2002.
XX 07-FEB-2002; 2002WO-BP001262.
XX 08-FEB-2001; 2001US-0267135P.
XX (FARB ) BAYER AG.
XX Zhu 2;
XX WPI; 2002-636596/68.
XX N-PSDB; AB222162, AB222164, AB222165.
XX New isolated human elongase HSELO1-like polynucleotide and encoded
PT peptide, useful for treating, preventing and ameliorating diseases such
PT as COPD, cancer, metabolic disease, diabetes, CNS disorders, or asthma.
XX PS
XX Claim 25; Fig 2; 128pp; English.
XX The present sequence represents a human elongase HSELO1-like protein (I).
XX (I) has cytostatic, antidiabetic, antiasthmatic, anti-HIV, nootropic,
XX antiparkinsonian, neuroprotective, tranquiliser, antiemetic, and can be used
XX analgesic, neuroleptic and cerebroprotective activities, and can be used
XX in gene therapy. (I) can be used in the treatment of a disease, such as
XX cancer, diabetes, central nervous system (CNS) disorder, asthma,
XX metabolic disease or COPD. The human elongase HSELO1-like protein is
XX useful in preventing, treating or ameliorating the diseases cited above,
XX including Parkinson's disease, dementia, multiple sclerosis, stroke, HIV,
XX Alzheimer's disease, Huntington's disease, Creutzfeldt-Jakob disease,
XX schizophrenia, psychosis, attention deficit disorders, pain associated
XX with CNS disorders, with cancer, or headache pain, e.g. migraine. It can
XX also be useful in identifying test compounds that may act as activators
XX or inhibitors at the enzyme's active site, or in raising specific
XX antibodies that can block and effectively reduce its activity
XX SQ
XX Sequence 270 AA;
Query Match 31.8%; Score 492; DB 5; Length 270;
Best Local Similarity 39.9%; Pred. No. 2e-45;
Matches 97; Conservative 53; Mismatches 87; Indels 6; Gaps 3;
QY 48 FOKYWHYSITISLVFLIKVIQKFMENRKPFTLKYPLILWNGALAAFSIATLRFSDIP 107
DB 30 FEYWATSPFIALIYLVLIAGVQNYMKERKGNLQGLILWSFCLAFSLGAVRWGMIM 89
QY 108 LRSLYABGFYKILCY-SCNPTDVAAPFWSFAPALS KIVELGDTMFIILRKPLIFLHYHH 166
DB 90 GTVLLTGLKQTCVCFINFDNSTVKFWSWFLSKVIELGDTAFIILRKPLIFLHYHH 149
QY 167 AAVLIYTHSGAEHTAAGRFYILMYFAHSLMYTYTTSVANGYRLPKWVSMVTVTQTTQ 226
DB 150 STVLVYTSFGYKYNKVPAGGFWFTMGVHAIWYTYTLKAAVYKPKMLPMLTSLQILQ 209
QY 227 MLAGVGITWVYKVKTEYKLPCCOOSVANLYLAFVIYVTFAILRFQFFVKAYI---IKSSK 283
DB 210 MFVGAIVSILTYIWRDQ--GCHTTMEHLFWSPILWYTYFILFAHFFCQYIIRPKVAKT 267
QY 284 KSK 286
DB 268 KSK 270
RESULT 10
ABB2960
ID ABB2960 standard; protein; 270 AA.
XX AC
XX ABB2960;
XX DT 14-APR-2003 (first entry)
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XX Human LCE related protein (sequence ID No. 10).
XX LCE; long chain fatty acyl elongase; p53; cytostatic; gene therapy;
XX cancer; human; enzyme.
XX Homo sapiens.
XX WO200299068-A2.
XX 12-DEC-2002.
XX 03-JUN-2002; 2002WO-US017739.
XX 05-JUN-2001; 2001US-0296076P.
XX 10-OCT-2001; 2001US-0328605P.
XX 15-FEB-2002; 2002US-0357253P.
XX 01-MAR-2002; 2002US-0361196P.
XX (EXEL-) EXELIXIS INC.
XX Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
XX Karim FD, Keyes LN, Koblizek TI;
XX WPI; 2003-167338/16.
XX Identifying a candidate p53 pathway modulating agent for
XX diagnosing/treating cancer comprises detecting a test agent-biased
XX activity of an assay system comprising a purified long chain fatty acyl
XX elongase (LCE) polypeptide or nucleic acid.
XX Claim 13; Page 60-61; 69pp; English.
XX The invention relates to identifying a candidate p53 pathway modulating
XX agent that involves assaying a purified LCE (long chain fatty acyl
XX elongase) polypeptide or nucleic acid or its functionally active fragment
XX or derivative, with a test agent. The methods are useful for identifying
XX a candidate p53 pathway modulating agent, modulating a p53 pathway of a
XX cell, or a mammalian cell, diagnosing a disease in a patient, identifying
XX a candidate branching morphogenesis modulating agent, and modulating
XX branching morphogenesis in a mammalian cell. The diseases that can be
XX diagnosed are breast, colon, lung or ovary cancer having greater than 25%
XX expression level. The method is useful for manufacturing a medicament for
XX diagnosing or treating breast, colon, lung or ovary cancer. Sequences
XX ABB2959-966 represent human LCE related polypeptide sequences
XX SQ
XX Sequence 270 AA;
Query Match 31.8%; Score 492; DB 6; Length 270;
Best Local Similarity 39.9%; Pred. No. 2e-45;
Matches 97; Conservative 53; Mismatches 87; Indels 6; Gaps 3;
QY 48 FOKYWHYSITISLVFLIKVIQKFMENRKPFTLKYPLILWNGALAAFSIATLRFSDIP 107
DB 30 FEYWATSPFIALIYLVLIAGVQNYMKERKGNLQGLILWSFCLAFSLGAVRWGMIM 89
QY 108 LRSLYABGFYKILCY-SCNPTDVAAPFWSFAPALS KIVELGDTMFIILRKPLIFLHYHH 166
DB 90 GTVLLTGLKQTCVCFINFDNSTVKFWSWFLSKVIELGDTAFIILRKPLIFLHYHH 149
QY 167 AAVLIYTHSGAEHTAAGRFYILMYFAHSLMYTYTTSVANGYRLPKWVSMVTVTQTTQ 226
DB 150 STVLVYTSFGYKYNKVPAGGFWFTMGVHAIWYTYTLKAAVYKPKMLPMLTSLQILQ 209
QY 227 MLAGVGITWVYKVKTEYKLPCCOOSVANLYLAFVIYVTFAILRFQFFVKAYI---IKSSK 283
DB 210 MFVGAIVSILTYIWRDQ--GCHTTMEHLFWSPILWYTYFILFAHFFCQYIIRPKVAKT 267
QY 284 KSK 286
DB 268 KSK 270
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OM protein - protein search, using sw model

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	492	31.8	270	10	US-09-976-782-18
3	492	31.8	270	10	US-09-976-782-20
4	492	31.8	270	16	US-10-433-238-9
5	485.5	31.4	278	9	US-09-903-456-58
6	485.5	31.4	278	14	US-10-156-911-58
7	485.5	31.4	278	14	US-10-408-736-56
8	479	31.0	271	9	US-09-903-456-53
9	479	31.0	271	10	US-09-976-782-107
10	479	31.0	271	14	US-10-156-911-53
11	479	31.0	271	14	US-10-408-736-50
12	479	31.0	272	9	US-09-903-456-24
13	479	31.0	272	14	US-10-156-911-24
14	479	31.0	272	14	US-10-408-736-21
15	476.5	30.8	261	9	US-09-903-456-60

Sequence 60, Appl
Sequence 58, Appl
Sequence 106, Appl
Sequence 37, Appl
Sequence 110, Appl
Sequence 64, Appl
Sequence 223, Appl
Sequence 239, Appl
Sequence 109, Appl
Sequence 4, Appl
Sequence 64, Appl
Sequence 62, Appl
Sequence 1115, Appl
Sequence 1114, Appl
Sequence 225, Appl
Sequence 108, Appl
Sequence 55, Appl
Sequence 89, Appl
Sequence 55, Appl
Sequence 89, Appl
Sequence 52, Appl
Sequence 56, Appl
Sequence 62, Appl
Sequence 56, Appl
Sequence 54, Appl
Sequence 60, Appl
Sequence 6094, Appl
Sequence 243, Appl
Sequence 20, Appl

US-10-369-493-5831
Sequence 5831, Application US/10369493
Publication No. US0030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5831
LENGTH: 291
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-10-369-493-5831

Query Match 100.0%; Score 1545; DB 15; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.7e-152; Indels 0; Gaps 0;
Matches 291; Conservative 0; Mismatches 0

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Db 1 MELAEFNDLNTFTIYGNPHDMMTKYKSYHPPGQVADPQYWTILFQKYVHSTISV 60
Qy 61 LYLILKVIQKFMENRKPFTLKYPLILWNGALAAFSIATLRFSDPLRLSYABGFYKTL 120
Db 61 LYLILKVIQKFMENRKPFTLKYPLILWNGALAAFSIATLRFSDPLRLSYABGFYKTL 120
Qy 121 CYSNPTDVAAPFWSAFALSKIVELGDMFTIILKRPFLIFLHYVTHAAVLIVYVHSGAEH 180

ALIGNMENTS

RESULT 1

US-10-369-493-5831
Sequence 5831, Application US/10369493
Publication No. US0030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5831
LENGTH: 291
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-10-369-493-5831

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Db	181	TAAGRFYILMNVPAHSLMY	TYTYS	AMGYRLPKVNSMTVT	TVQTOMLAGVGI	TWVYKV 240
Qy	241	KTEYKLPCQOSVANILYLA	FVIVT	PAILFI	QFFVKAVIIKSSKKS	SVQNE 291
Db	241	KTEYKLPCQOSVANILYLA	FVIVT	PAILFI	QFFVKAVIIKSSKKS	SVQNE 291

RESULT 2

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US-09-976-782-18
; Sequence 18, Application US/09976782
; Publication No. US20030190715A1
; GENERAL INFORMATION:
; APPLICANT: Grosse et al
; TITLE OF INVENTION: No. US20030190715A1e1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-157
; CURRENT APPLICATION NUMBER: US/09/976,782
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,113
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,662
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,732
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,625
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,703
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/241,190
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,637
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,669
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/262,455
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/240,648
; PRIOR FILING DATE: 2000-10-16
; NUMBER Of SEQ ID NOS: 127
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 18
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-976-782-18

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RESULT 4

US-10-433-238-9
RESOL 4
; Sequence 9, Application US/10433238
; Publication NO. US20040086899A1
; GENERAL INFORMATION:
; APPLICANT: Wintier, Michael D
; APPLICANT: Knickle, Leah C
; APPLICANT: Haardt, Martin
; APPLICANT: Allen, Stephen J

RESULT 3
US-09-976-782-20
; Sequence 20, Application US/09976782
; Publication No. US20030190715A1
; GENERAL INFORMATION:

Query Match	31.8%;	Score 492;	DB 10;	Length 270;
Best Local Similarity	39.9%;	Pred. No. 8.6e-43;		
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QY	48	FOKXWYHSITISVLVYFILIKVIQKFMENRKPFTILKYPLILMNGALAAFSIIATLRFSDIP	107	
DB	30	FEETWATSPFALILYLVLLAVGQVNYMKERGFNLQGPLLWSPCLATPSILCAVMMGIM	89	
QY	108	LRSLYASGFYKTLCY - SCNPYDVAAFPNSFAPALSKIVELGDTMTILILKRPLILPHVYHH	166	
DB	90	GTVLTLGGLKOTVCFINPIDSNTVKFWSWVELLSKVIELGDTAFILILKRPLILPHVYHH	149	
QY	167	AAVLIVTTHVHSGAETHAAGRFILMLNYFAHSLMYYTYTVSANGYELPKWVSMVTIVTQTO	226	
DB	150	STVLVYTSFGYKKNKVPAGGMVPTWNGFVHAIMYTYTILKAANVKPPKMLPLIITSLQILQ	209	
QY	227	MLAGVIGITWMYKYKTEYKLPQOOSVANLYLAFVITYTFAILTFQGFVKAYI - - - IKSSK	283	
DB	210	MFVGAIVSILTYIWRDQO - - GCHTITMEHLFWSPILDMYFILPHAFHFCQTYIRPKVKAKT	267	
QY	284	KSK	286	
DB	268	KSO	270	

RESULT 4

RESOL 4
US-10-433-238-9
; Sequence 9, Application US/10433238
; Publication NO. US20040086899A1
; GENERAL INFORMATION:
; APPLICANT: Wintier, Michael D
; APPLICANT: Knickle, Leah C
; APPLICANT: Haardt, Martin
; APPLICANT: Allen, Stephen J

```

; APPLICANT: Ponton, Andre
; APPLICANT: De Antueno, Roberto J
; APPLICANT: Jenkins, D K
; APPLICANT: Nwaka, Solomon O
; APPLICANT: Goldberg, Y Paul
; TITLE OF INVENTION: Human Elongase Genes, Uses Thereof, and Compounds for
; TITLE OF INVENTION: Modulating Same
; FILE REFERENCE: 330339-00004
; CURRENT APPLICATION NUMBER: US/10/433,238
; PRIOR FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: US 60/253,728
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 270
; TYPE: PRT
; ORGANISM: human
US-10-433-238-9

Query Match      31.8%; Score 492; DB 16; Length 270;
Best Local Similarity 39.9%; Pred. No. 8.6e-43;
Matches 97; Conservative 53; Mismatches 87; Indels 6; Gaps 3;

Qy 48 FOKYVHSTISVLVLIKVKQKEMENRKPPTLKVPLILWNGALAAFSIATLRFSDIP 107
Db 30 FEEYATSPPIALIVLIVLAVGQNTWKERKGNLQOPILILNSFCLAIISILCAVRMNGIM 89

Qy 108 LRSVLAEGFYKTCY-SCNPTDVAAPFWSFAFALSXIVELGDTMPILRRPLIFLHYHH 166
Db 90 GIVLLTGGLKQVCFINFDNSTVRFWSWVFLSKVIELGDTAFILRRPLIF-HWYEH 149

Qy 167 AAVLYTVHSGAEHTAAGFYILMYFAHSLMYTVYSAMCYRLPKVSMVTVTQTO 226
Db 150 STVLVYTSFGYKXKVPAGGFVTFMFGVHAINVYITLKAANKPKMLDFMITSLSLILQ 209

Qy 227 MLAGVGITVMVYKTEYKLPQQSVANLYAFVIVYTFAILFIOFFVKAYI---IKSK 283
Db 210 MFVGAIVSLITVWRQDQ--GCHTWEHLFWFSLVIMYFIFLFAHFFCQYIRPKVAKT 267

Qy 284 KSK 286
Db 268 KSG 270

RESULT 5
US-09-903-456-58
; Sequence 58, Application US/09903456
; Patent No. US20020138874A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (235)... (235)
; OTHER INFORMATION: Xaa = Unknown or Other at position 235
US-10-156-911-58

Query Match      31.4%; Score 485.5; DB 14; Length 278;
Best Local Similarity 37.7%; Pred. No. 4.3e-42;
Matches 103; Conservative 54; Mismatches 99; Indels 17; Gaps 5;

Qy 23 MTTKYKSYHFPGEQVADP-----QYWTILFQKYWHTSITISVLVYFILIKVIOKFMENR 76
Db 11 VTPNYSYIFDFENDFIHQTRKWMLENWTWVF---YYCGI-----YMLVIFGGQHFMQNR 62

Qy 77 KPFTLKYPILWNGALAAFSIATLRFSDIPSLRSVLAEGFYKTCYS--CNPTDVAAPFWS 134
Db 63 PRFOLRGPLIWNLLANFSLMGARTAPSLIHVLRHYGLFHSVCVPSYIEQDRVCGFWT 122

Qy 135 FAFALSXIVELGDTMPILRRPLIFLHYHHAAVLYTVHSGAEHTAAGFYILMYFA 194
Db 123 WLFVLSKLPGLGDTFIVLRKQPLIFLHYHHITVLIYSWFSYTEYTSARWFIWMYCV 182

Qy 195 HSLMYTVYSAMCYRLPKVSMVTVTQTOMLAGVGI-TMVYKVKTEYKLPQQQSV 253
Db 183 HSNMYSYALKAAAFNPRFISMITSLSLAQMIIGCAINWANGFLKTHGTXSCHLSQR 242

Qy 254 NLYLAFVIVYTFAILFIOFFVKAYIIEKSKSK 286
Db 243 NINLSIAMYSYFVLFARFFYKAYLAPGCHKSR 275

RESULT 6
US-10-156-911-58
; Sequence 58, Application US/10156911
; Publication No. US20030163845A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P4
; CURRENT APPLICATION NUMBER: US/10/156,911
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 09/903,456
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (235)... (235)
; OTHER INFORMATION: Xaa = Unknown or Other at position 235
US-10-156-911-58

Query Match      31.4%; Score 485.5; DB 14; Length 278;
Best Local Similarity 37.7%; Pred. No. 4.3e-42;
Matches 103; Conservative 54; Mismatches 99; Indels 17; Gaps 5;

Qy 23 MTTKYKSYHFPGEQVADP-----QYWTILFQKYWHTSITISVLVYFILIKVIOKFMENR 76
Db 11 VTPNYSYIFDFENDFIHQTRKWMLENWTWVF---YYCGI-----YMLVIFGGQHFMQNR 62

Qy 77 KPFTLKYPILWNGALAAFSIATLRFSDIPSLRSVLAEGFYKTCYS--CNPTDVAAPFWS 134
Db 63 PRFOLRGPLIWNLLANFSLMGARTAPSLIHVLRHYGLFHSVCVPSYIEQDRVCGFWT 122
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; LOCATION: (235)... (235)
; OTHER INFORMATION: Xaa = Unknown or Other at position 235
US-09-903-456-58

Query Match      31.4%; Score 485.5; DB 9; Length 278;
Best Local Similarity 37.7%; Pred. No. 4.3e-42;
Matches 103; Conservative 54; Mismatches 99; Indels 17; Gaps 5;

Qy 23 MTTKYKSYHFPGEQVADP-----QYWTILFQKYWHTSITISVLVYFILIKVIOKFMENR 76
Db 11 VTPNYSYIFDFENDFIHQTRKWMLENWTWVF---YYCGI-----YMLVIFGGQHFMQNR 62

Qy 77 KPFTLKYPILWNGALAAFSIATLRFSDIPSLRSVLAEGFYKTCYS--CNPTDVAAPFWS 134
Db 63 PRFOLRGPLIWNLLANFSLMGARTAPSLIHVLRHYGLFHSVCVPSYIEQDRVCGFWT 122

Qy 135 FAFALSXIVELGDTMPILRRPLIFLHYHHAAVLYTVHSGAEHTAAGFYILMYFA 194
Db 123 WLFVLSKLPGLGDTFIVLRKQPLIFLHYHHITVLIYSWFSYTEYTSARWFIWMYCV 182

Qy 195 HSLMYTVYSAMCYRLPKVSMVTVTQTOMLAGVGI-TMVYKVKTEYKLPQQQSV 253
Db 183 HSNMYSYALKAAAFNPRFISMITSLSLAQMIIGCAINWANGFLKTHGTXSCHLSQR 242

Qy 254 NLYLAFVIVYTFAILFIOFFVKAYIIEKSKSK 286
Db 243 NINLSIAMYSYFVLFARFFYKAYLAPGCHKSR 275

RESULT 6
US-10-156-911-58
; Sequence 58, Application US/10156911
; Publication No. US20030163845A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P4
; CURRENT APPLICATION NUMBER: US/10/156,911
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 09/903,456
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (235)... (235)
; OTHER INFORMATION: Xaa = Unknown or Other at position 235
US-10-156-911-58

Query Match      31.4%; Score 485.5; DB 14; Length 278;
Best Local Similarity 37.7%; Pred. No. 4.3e-42;
Matches 103; Conservative 54; Mismatches 99; Indels 17; Gaps 5;

Qy 23 MTTKYKSYHFPGEQVADP-----QYWTILFQKYWHTSITISVLVYFILIKVIOKFMENR 76
Db 11 VTPNYSYIFDFENDFIHQTRKWMLENWTWVF---YYCGI-----YMLVIFGGQHFMQNR 62

Qy 77 KPFTLKYPILWNGALAAFSIATLRFSDIPSLRSVLAEGFYKTCYS--CNPTDVAAPFWS 134
Db 63 PRFOLRGPLIWNLLANFSLMGARTAPSLIHVLRHYGLFHSVCVPSYIEQDRVCGFWT 122
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Db 63 PRFQRLGELIWNILLAMPSIMGAARTAPELIHVLRHYGLFHSVCVPSYIEQDRVCGFWT 122
QY 135 PAFALSKIVELGDTWFIILKRPFLFLHYHAAVLIVTVHSGAEHTAAGREYILMNYFA 194
Db 123 WLFVLSKPELGDITFIVLRKQPLIFLWYHHITVLIYSWFSYTYETSSARFIWNYCV 182
QY 195 HSLMVTYTVSAMGYRLPKWNSMTVTQVQTMLAGVGI-TWVYKVKTEYKXLPCCQSV 253
Db 183 HSNVSYALKAAFPNPFISMIITSLQ-AMIIIGCAINWANGFLKTHGTXSCHISOR 242
QY 254 NLYAFVYVTTAILFIQFVKAYIIKSKSK 286
Db 243 NINLSIAMYSYVFLFARFFKAYLAPGGHKS 275

RESULT 7

US-10-408-736-56
; Sequence 56, Application US/10408736
; Publication No. US20030177508A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Das, Tapas
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Parker-Barnes, Jennifer M.
; APPLICANT: Leonard, Amanda Eun-yeong
; APPLICANT: Thurmond, Jennifer M.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P1
; CURRENT APPLICATION NUMBER: US/10/408,736
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US/09/379,095A
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (235)...(235)
; OTHER INFORMATION: Xaa = Unknown or Other at position 235
US-10-408-736-56

Query Match 31.4%; Score 485.5; DB 14; Length 278;
Best Local Similarity 37.7%; Pred. No. 4.3e-42;
Matches 103; Conservative 54; Mismatches 99; Indels 17; Gaps 5;

QY 23 MTKYKYSYHPPGEOVADP-----QYMTILFQKYWYHSITISVLVFIKIKVQKEMNR 76
Db 11 VTPNYSYIFDFNDHFHQRTRKMKLENWTVF---YYCGI-----YMLVIFGQGHQNR 82
QY 77 KPFTLKYPILWNGALAAFSIIATLRSIDPLSLVAGFYKTLCS--CNPTDVAAPWS 134
Db 63 PRFQRLGELIWNILLAMPSIMGAARTAPELIHVLRHYGLFHSVCVPSYIEQDRVCGFWT 122
QY 135 PAFALSKIVELGDTWFIILKRPFLFLHYHAAVLIVTVHSGAEHTAAGREYILMNYFA 194
Db 123 WLFVLSKPELGDITFIVLRKQPLIFLWYHHITVLIYSWFSYTYETSSARFIWNYCV 182
QY 195 HSLMVTYTVSAMGYRLPKWNSMTVTQVQTMLAGVGI-TWVYKVKTEYKXLPCCQSV 253
Db 183 HSNVSYALKAAFPNPFISMIITSLQ-AMIIIGCAINWANGFLKTHGTXSCHISOR 242
QY 254 NLYAFVYVTTAILFIQFVKAYIIKSKSK 286
Db 243 NINLSIAMYSYVFLFARFFKAYLAPGGHKS 275

RESULT 8

US-09-903-456-53
; Sequence 53, Application US/09903456
; Patent No. US20020138874A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-903-456-53

Query Match 31.0%; Score 479; DB 9; Length 271;
Best Local Similarity 41.6%; Pred. No. 2e-41; 87; Indels 8; Gaps 4;
Matches 101; Conservative 47; Mismatches 47;

QY 49 QKQWYHSITISVLVFIKIKVQKEMNRKFTLKYPILWNGALAAFSIIATLRSIDPL 108
Db 32 EYTWSSPLIVVYLLIVVGVQYMRTRKSPQLRPLILWSFPLAIFSILGTLRMKFWA 91
QY 109 RSLVAGFYKTLCSNPTD-VAAFWSPALSKIVELGDTWFIILKRPFLFLHYHHA 167
Db 92 TVMTVGLKQTCVFAIYTDADVRFVSEFLFLSKVVELGDTAFILIRKPLIFVWYHHS 151
QY 168 AVLIVTVHSGAEHTAAGREYILMNYFAHSLMVTYTVSAMGYRLPKWNSMTVTQVQTM 227
Db 152 TVLFTSFGYKKNKVPSPGGWMTNFGVHSVMVYTYTMAAKLKHNPILPMTSLQILQM 211
QY 228 LAGV--GITWVYKVKTEYKLPCCQSVANLYAFVYVTTAILFIQFVKAYIIKSSK-K 284
Db 212 VLGTIFGILNYIR---QEKGCHTTEHFFNSFMYLGYTIFLFAHFFHAYLRPKGVA 267
QY 285 SKS 287
Db 268 SKS 270

RESULT 9

US-09-976-782-107
; Sequence 107, Application US/09976782
; Publication No. US20030190715A1
; GENERAL INFORMATION:
; APPLICANT: Grosse et al
; TITLE OF INVENTION: No. US20030190715A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-157
; CURRENT APPLICATION NUMBER: US/09/976,782
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,113
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,662
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,732
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,625
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,703
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/241,190

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; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,637
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,669
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/262,455
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/240,648
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-782-107

Best Local Similarity 31.0%; Score 479; DB 10; Length 271;
Matches 101; Conservative 47; Mismatches 87; Indels 8; Gaps 4;

QY 49 QKYWHSITISVLYFIIKVIQKFMENKXPTLKYPILWNGALAAFSIIATLRPSIDPL 108
DB 32 BEYVSSFLIVVYLLIIVGQTYMTRKSPSFLQRPILWSPFLAIPFSLGTLRMWKPMA 91
QY 109 RSLYAEGFYKTLCYSCNPTD-VAAFWSPAFALSKIVELGDTMFIILRKRPILFLHYHHA 167
DB 92 TVMFTVGLKQTVCPAIYTDADVRFWSFLSKVVELGDTAFIILRKRPILFLHYHHA 151
QY 168 AVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYTYSAMGYRLPKWVSMVTVTQTOM 227
DB 152 TVLLFTSFGYKKNKVPSCGWFMTMNFVGHVSVMTYTTKAAKLKHPNLLPMWITSILQILQM 211
QY 228 LAGV--GITMVMYKVKTEYKLPCCQSVANLYLAFVIYVTFAILFQFFVKAYIIKSSK-K 284
DB 212 VLGTFIGILNYIWR-----QKGCHTTTEHFFWSFNLGYTYFILFAHFFHRAIYLRPKGVA 267
QY 285 SKS 287
DB 268 SKS 270

RESULT 11
US-10-408-736-50
; Sequence 50, Application US/10408736
; Publication No. US20030177508A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Das, Tapas
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Parker-Barnes, Jennifer M.
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Thurmond, Jennifer M.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P1
; CURRENT APPLICATION NUMBER: US/10/408,736
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US/09/379,095A
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-408-736-50

Query Match 31.0%; Score 479; DB 14; Length 271;
Best Local Similarity 41.6%; Pred. No. 2e-41;
Matches 101; Conservative 47; Mismatches 87; Indels 8; Gaps 4;

QY 49 QKYWHSITISVLYFIIKVIQKFMENKXPTLKYPILWNGALAAFSIIATLRPSIDPL 108
DB 32 BEYVSSFLIVVYLLIIVGQTYMTRKSPSFLQRPILWSPFLAIPFSLGTLRMWKPMA 91
QY 109 RSLYAEGFYKTLCYSCNPTD-VAAFWSPAFALSKIVELGDTMFIILRKRPILFLHYHHA 167
DB 92 TVMFTVGLKQTVCPAIYTDADVRFWSFLSKVVELGDTAFIILRKRPILFLHYHHA 151
QY 168 AVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYTYSAMGYRLPKWVSMVTVTQTOM 227
DB 152 TVLLFTSFGYKKNKVPSCGWFMTMNFVGHVSVMTYTTKAAKLKHPNLLPMWITSILQILQM 211
QY 228 LAGV--GITMVMYKVKTEYKLPCCQSVANLYLAFVIYVTFAILFQFFVKAYIIKSSK-K 284
DB 212 VLGTFIGILNYIWR-----QKGCHTTTEHFFWSFNLGYTYFILFAHFFHRAIYLRPKGVA 267
QY 285 SKS 287

Query Match 31.0%; Score 479; DB 14; Length 271;
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; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,637
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,669
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/262,455
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/240,648
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-782-107

Best Local Similarity 41.6%; Pred. No. 2e-41;
Matches 101; Conservative 47; Mismatches 87; Indels 8; Gaps 4;

QY 49 QKYWHSITISVLYFIIKVIQKFMENKXPTLKYPILWNGALAAFSIIATLRPSIDPL 108
DB 32 BEYVSSFLIVVYLLIIVGQTYMTRKSPSFLQRPILWSPFLAIPFSLGTLRMWKPMA 91
QY 109 RSLYAEGFYKTLCYSCNPTD-VAAFWSPAFALSKIVELGDTMFIILRKRPILFLHYHHA 167
DB 92 TVMFTVGLKQTVCPAIYTDADVRFWSFLSKVVELGDTAFIILRKRPILFLHYHHA 151
QY 168 AVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYTYSAMGYRLPKWVSMVTVTQTOM 227
DB 152 TVLLFTSFGYKKNKVPSCGWFMTMNFVGHVSVMTYTTKAAKLKHPNLLPMWITSILQILQM 211
QY 228 LAGV--GITMVMYKVKTEYKLPCCQSVANLYLAFVIYVTFAILFQFFVKAYIIKSSK-K 284
DB 212 VLGTFIGILNYIWR-----QKGCHTTTEHFFWSFNLGYTYFILFAHFFHRAIYLRPKGVA 267
QY 285 SKS 287

Query Match 31.0%; Score 479; DB 14; Length 271;
Best Local Similarity 41.6%; Pred. No. 2e-41;
Matches 101; Conservative 47; Mismatches 87; Indels 8; Gaps 4;

QY 49 QKYWHSITISVLYFIIKVIQKFMENKXPTLKYPILWNGALAAFSIIATLRPSIDPL 108
DB 32 BEYVSSFLIVVYLLIIVGQTYMTRKSPSFLQRPILWSPFLAIPFSLGTLRMWKPMA 91
QY 109 RSLYAEGFYKTLCYSCNPTD-VAAFWSPAFALSKIVELGDTMFIILRKRPILFLHYHHA 167
DB 92 TVMFTVGLKQTVCPAIYTDADVRFWSFLSKVVELGDTAFIILRKRPILFLHYHHA 151
QY 168 AVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYTYSAMGYRLPKWVSMVTVTQTOM 227
DB 152 TVLLFTSFGYKKNKVPSCGWFMTMNFVGHVSVMTYTTKAAKLKHPNLLPMWITSILQILQM 211
QY 228 LAGV--GITMVMYKVKTEYKLPCCQSVANLYLAFVIYVTFAILFQFFVKAYIIKSSK-K 284
DB 212 VLGTFIGILNYIWR-----QKGCHTTTEHFFWSFNLGYTYFILFAHFFHRAIYLRPKGVA 267
QY 285 SKS 287
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Wed Jun 16 16:10:39 2004

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DB      268 SKS 270

RESULT 12
US-09-903-456-24
; Sequence 24, Application US/09903456
; Patent No. US20020138874A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: US 09/145,828
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (272)...(272)
; OTHER INFORMATION: Xaa = Unknown or Other at position 272
US-09-903-456-24

Query Match      31.0%; Score 473; DB 9; Length 272;
Best Local Similarity 41.6%; Pred. No. 2e-41;
Matches 101; Conservative 47; Mismatches 87; Indels 8; Gaps 4;

QY 49 QKWWHSITISLVLYFIKVIQKFMENRKPFTLKYPILNGLAALAFSIIATLRFSDPL 108
DB 32 EEWVSSFLIVVYLLLVGGTYMTRKFSIQRLILWSFFLAIFSILGTLRWKFWA 91
QY 109 RSLYAGFYKTLVCYNPTD-VAAFWSPAFALSKIVELGDTMFIILRRPLIFLHYHHA 167
DB 92 TMTFTVGLKQVCFALYTDVAVRFSFLSKVVELGDTAFILLRKPLIFVHWYHS 151
QY 168 AVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYTYSAMGYRLPKWVSMVTVTQTOM 227
DB 152 TVLLFTSFGYKKNVPSGCFWMTNFGVHSMVYTYTAKAKLKHPLLPKMTLSLQILQM 211
QY 228 LAGV--GITWVYKVKTEYKLPQQSVANLYLAFVIYVTFALFIQFPVKAYTIKSSK-K 284
DB 212 VLGTIFGILNYWR-----QKGGCHTTTEHFFWSEFMYLGYTYFILFAHFFHRAVLRPKGVA 267
QY 285 SKS 287
DB 268 SKS 270

RESULT 14
US-10-408-736-21
; Sequence 21, Application US/10408736
; Publication No. US20030177508A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Das, Tapas
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Parker-Barnes, Jennifer M.
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Thurmond, Jennifer M.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P1
; CURRENT APPLICATION NUMBER: US/10/408,736
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US/09/379,095A
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Mus musculus

QY 49 QKWWHSITISLVLYFIKVIQKFMENRKPFTLKYPILNGLAALAFSIIATLRFSDPL 108
DB 32 EEWVSSFLIVVYLLLVGGTYMTRKFSIQRLILWSFFLAIFSILGTLRWKFWA 91
QY 109 RSLYAGFYKTLVCYNPTD-VAAFWSPAFALSKIVELGDTMFIILRRPLIFLHYHHA 167
DB 92 TMTFTVGLKQVCFALYTDVAVRFSFLSKVVELGDTAFILLRKPLIFVHWYHS 151
QY 168 AVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYTYSAMGYRLPKWVSMVTVTQTOM 227
DB 152 TVLLFTSFGYKKNVPSGCFWMTNFGVHSMVYTYTAKAKLKHPLLPKMTLSLQILQM 211
QY 228 LAGV--GITWVYKVKTEYKLPQQSVANLYLAFVIYVTFALFIQFPVKAYTIKSSK-K 284
DB 212 VLGTIFGILNYWR-----QKGGCHTTTEHFFWSEFMYLGYTYFILFAHFFHRAVLRPKGVA 267
QY 285 SKS 287
DB 268 SKS 270

RESULT 13
US-10-156-911-24
; Sequence 24, Application US/10156911
; Publication No. US20030163845A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P4
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; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (272)...(272)
; OTHER INFORMATION: Xaa = Unknown or Other at position 272
US-10-408-736-21

Query Match      31.0%; Score 479; DB 14; Length 272;
Best Local Similarity 41.6%; Pred. No. 2e-41;
Matches 101; Conservative 47; Mismatches 87; Indels 8; Gaps 4;

QY 49 QKYWHSTISVLYFILLIKVQKFNKPTLKYPLILWNGALAAFSIIATLRFSDPL 108
DB 32 EEWVSSEFLIVVYLLLVGGTYMRTRKSPSLQRPILWSPFLAIPSLGLTKRWKEMA 91
QY 109 RSLVAEGFYKILCYSCNPTD-VAAFWSPAFALSKIVELGDTMFIILRKRPILFLHYHHA 167
DB 92 TWMTFTVLGLKQVCFPAIYDDAVRFSFLFLSKVVELGDTAFIILRKRPILFVHWYHHS 151
QY 168 AVLIYTVHSGAHTFAAGFYILMNYFAHSLMYTYTYSAMGYRLPKWYMTVTVTOTOM 227
DB 152 TVLLFTSEGYKNKVPSCGFMFTMFGVHSMVYTYTMAAKLKHFNLLPMTVITSLQILQM 211
QY 228 LAGV-GITWVYKVKTEYKLPQCOOSVANLYLAFVIYVTFAILFTQPFVKAYIHKSSK-K 284
DB 212 VLGTFPGILNYWR----QEKCHTTEHFFNSFMYLGYTFILFAHFFHRAVLYREKQVA 267
QY 285 SKS 287
DB 268 SKS 270
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Search completed: June 16, 2004, 15:34:59
Job time : 49 secs

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RESULT 15
US-09-903-456-60
; Sequence 60, Application US/09903456
; Patent No. US2002013874A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Sun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1998-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (218)...(218)
; OTHER INFORMATION: Xaa = Unknown or Other at position 218
US-09-903-456-60

Query Match      30.8%; Score 476.5; DB 9; Length 261;
Best Local Similarity 40.2%; Pred. No. 3.4e-41;
Matches 99; Conservative 49; Mismatches 87; Indels 11; Gaps 4;

QY 44 WTILFQKYWHSTISVLYFILLIKVQKFNKPTLKYPLILWNGALAAFSIIATLRF 103
DB 21 WTWVP---YYCGI-----YMLVIFGGQHTFQNRPRFQLGPLIIMTWLLANFSIMGAFT 72
QY 104 SIDPLRSLVAEGFYKILCYSCNPTDVAAFNSFALSKIVELGDTMFIILRKRPILFL 161
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2004, 15:25:29 ; Search time 21 Seconds
(without alignments)
1332.940 Million cell updates/sec

Title: US-09-936-845A-15
Perfect score: 1545
Sequence: 1 MELAEFNDLNTFTTYGNH.....PFVKAYIIKSKKSKSVKNE 291

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1545	100.0	291	2 S28299	hypothetical prote
2	564	36.5	435	2 T34200	hypothetical prote
3	398	25.8	274	2 T20786	hypothetical prote
4	374	24.2	274	2 H88690	protein F41H10.8
5	360	23.3	288	2 T22789	hypothetical prote
6	329	21.3	281	2 T22791	hypothetical prote
7	327.5	21.2	286	2 B88690	protein F41H10.7
8	281.5	18.2	328	2 T37734	SUR4 family protei
9	262	17.0	345	2 S48517	SUR4 protein - yea
10	235.5	15.2	334	2 T50139	GNS1/SUR4 family p
11	220.5	14.3	310	2 S46638	probable membrane
12	220	14.2	347	2 S12916	hypothetical prote
13	191	12.4	158	2 T46257	hypothetical prote
14	128.5	8.3	868	2 T31527	protein Putative A
15	117.5	7.6	1435	2 D96693	hypothetical prote
16	117	7.6	281	2 H96779	arginine/ornitine
17	111.5	7.2	497	2 G86878	nitric oxide reduc
18	109.5	7.1	448	2 AH3095	nitric oxide reduc
19	109.5	7.1	448	2 B98191	cellulose synthase
20	105	6.8	729	2 A98320	cellulose synthase
21	105	6.8	729	2 AD2963	cellulose synthase
22	105	6.8	861	2 T39714	hypothetical prote
23	103.5	6.7	330	2 T22293	conserved hypothet
24	102	6.6	880	2 D69427	probable carnitine
25	99.5	6.4	510	2 G71365	hypothetical prote
26	99.5	6.4	919	2 S37786	nitric-oxide reduc
27	98.5	6.4	443	2 AE3634	ATP/ADP translocas
28	97.5	6.3	498	1 JQ0026	probable ABC-type
29	97	6.3	219	2 P81365	

30 96.5 6.2 272 2 T11689
31 96 6.2 474 2 S41117
32 95.5 6.2 407 2 D86782
33 95 6.1 782 2 E90427
34 95 6.1 2671 2 A49873
35 94 6.1 271 2 T11692
36 94 6.1 306 2 AC1174
37 93.5 6.1 759 2 A46188
38 93 6.0 423 2 A90450
39 92.5 6.0 448 2 F95348
40 92 6.0 291 2 T31962
41 92 6.0 308 2 AD1531
42 92 6.0 750 2 B83794
43 92 6.0 952 2 AG1209
44 91.5 5.9 289 2 C69346
45 91.5 5.9 321 2 E90492

ALIGNMENTS

RESULT 1

S28299
hypothetical protein C40H1.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Sep-1997
C;Accession: S28299
submitted to the EMBL Data Library, December 1992
R;Berkx, M.
A;Reference number: S28296
A;Accession: S28299
A;Molecule type: DNA
A;Residues: 1-291 <BER>
A;Cross-references: EMBL:Z19154; NID:G6650; PID:G6654
C;Genetics:
A;Introns: 30/2; 68/1; 105/3; 177/1
C;Keywords: transmembrane protein

Query Match 100.0%; Score 1545; DB 2; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELAEFNDLNTFTTYGNHDTMTTKYKSYHFFGEQVADPOYTWILFKYHYHSHITISV 60
DB 1 MELAEFNDLNTFTTYGNHDTMTTKYKSYHFFGEQVADPOYTWILFKYHYHSHITISV 60
QY 61 LYFILIKVQKFMENRKPTLYKYLILNKGALAAFSIATLRFSDPLRSLVAEGFYKTL 120
DB 61 LYFILIKVQKFMENRKPTLYKYLILNKGALAAFSIATLRFSDPLRSLVAEGFYKTL 120
QY 121 CYSCNPTDVAATPWSAFALSKIVELGDTMFIILKRKPLFLHYHHAAYLIYTVHSGAEH 180
DB 121 CYSCNPTDVAATPWSAFALSKIVELGDTMFIILKRKPLFLHYHHAAYLIYTVHSGAEH 180
QY 181 TAAGRPYILMNTFAHSLMNTYTVSANGYRLPKWYSMTVTVTQTTOMLAGVGTWVYKV 240
DB 181 TAAGRPYILMNTFAHSLMNTYTVSANGYRLPKWYSMTVTVTQTTOMLAGVGTWVYKV 240
QY 241 KTEYKLPCCQSVANLYLAFVIYVTFALFIQFFVKAYIIKSKKSKSVKNE 291
DB 241 KTEYKLPCCQSVANLYLAFVIYVTFALFIQFFVKAYIIKSKKSKSVKNE 291

RESULT 2

T34200
hypothetical protein D2024.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
R;Du, Z.; Gattung, S.
C;Accession: T34200
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid D2024.
A;Reference number: Z21488

A;Accession: T34200
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-435 <DUZ>
A;Cross-references: EMBL:U41011; PIDN:AAA82288.1; CESP:D2024.3
C;Genetics:
A;Introns: 17/3; 57/3; 306/1; 398/3

Query Match 36.5%; Score 564; DB 2; Length 435;
Best Local Similarity 42.0%; Pred. No. 4.9e-42;
Matches 128; Conservative 45; Mismatches 86; Indels 46; Gaps 7;

QY 22 DMTTKY---KSYHFGEQVADPQYWTILFQKYWHSITISVLYFILI-----KVI-----69
Db 5 DYNPKVLENSYIFLPETSDAFRSTWQNEHWQISITASVYVAVIFPGKVVLIYKK 64
QY 70 -----QKF--MENRKPFLKYPLILANGALAAFSIATLR 102
Db 65 SRVITPFISSIONAQRNRKSLANSSOMFQIKPKPQDTPLPVWNSFLAIFSIILFLR 124
QY 103 FSDIDPLRSLYAEG--FYKTLCSYCNPTDVAAFWSFAPALSKIIVELGDTWFIILRKRLPIF 160
Db 125 MTEFVWSNABEGNSFKYSICHSSYAGVGTGFWTEQFANSKLFELIDTIFIVLRKRLPIF 184
QY 161 LHYTHAAVLIYTHSGAETHRAGRFLIMNYFAHSLMYTYTVSANGYELPKVWSMTVT 220
Db 185 LHWYHVTVMYITWYHAYKHTASGRWFIWNYGVHAWMSYALRSUKFLPKQMAWVT 244
QY 221 TVQTTOMLAGVGTIMWYKVKTI--EYKLPQQQSVANLYLAFVIYVTFPAIFIOFFVKAYI 278
Db 245 TLQALQWVGVIIGTVYIRKSGEY---CQQTWDLNGLCGVYFTYFLFANFFYHAYV 301
QY 279 IKSSK 283
Db 302 KQNR 306

RESULT 3
T20786
hypothetical protein F11B6.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20786
R;Matthews, L.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19324
A;Accession: T20786
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-274 <WIL>
A;Cross-references: EMBL:Z81058; PIDN:CAB02921.1; GSPDB:GN00022; CESP:F11B6.5
C;Genetics:
A;Gene: CESP:F11B6.5
A;Map position: 4
A;Introns: 38/3; 99/1; 183/2; 235/2

Query Match 25.8%; Score 398; DB 2; Length 274;
Best Local Similarity 37.1%; Pred. No. 1.2e-27;
Matches 89; Conservative 48; Mismatches 99; Indels 4; Gaps 4;

QY 55 S TISVLYFILIYKIQKPMENRKPFTLKYPLILANGALAAFSIATLRFSIDPLRSIYAE 114
Db 36 SYKIMIGVLTIVFGQKLMARHKPDLQNTLALNFGFLSFGIAAYKLIPELFGVPMKD 95
QY 115 GFYKTLCSYCN-PTDVA-AFWSFAPALSKIIVELGDTWFIILRKRLPIFLHYHAAVLIY 172
Db 96 GFVASVQENNYTDASTGFGWAFVMSKAPELGDTWFLVRKPFVIFMWHYHALTFVY 155
QY 173 TVHSGAETHRAGRFLIMNYFAHSLMYTYTVSANGYELPKVWSMTVTQTTOMLAGV 232
Db 156 AVWTYSEHQAWRWSLALNLAHVITWYFYFAVRALNIQTFRFVAKFITTIQIVQVISCY 215

QY 233 ITMWYKVKTYKLP-CQOSVANLYLAFVIYVTFPAIFIOFFVKAYIILKSKSKSVKNE 291
Db 216 IPGHLVFIKSADSVPGCAVSNVLSIGLGLVYISLFLFAKFFKAYIQGRS-PTKTSKOB 274

RESULT 4
H88690
protein F41H10.8 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
A;Accession: H88690
R;Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biol
A;Reference number: A75000; MDID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/c_elegans/ and www.sanger.ac.uk/Projects/C_el
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; at
A;Accession: H88690
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-274 <STO>
A;Cross-references: GB:chr_IV; PIDN:AAB03175.1; PID:gl397336; GSPDB:GN00022; CESP:F41H1
C;Genetics:
A;Gene: F41H10.8
A;Map position: 4

Query Match 24.2%; Score 374; DB 2; Length 274;
Best Local Similarity 30.4%; Pred. No. 1.6e-25;
Matches 83; Conservative 59; Mismatches 111; Indels 20; Gaps 6;

QY 22 DMTTKYKSYHFGEQVADPQYWTILFQKYWHSITISVLYFILIYKIVIOKFMENRKPFTL 81
Db 10 EVLITAPPSELSKXHIATQY-----AAFW-----ISMAYVVIIFGLKAVMTNRKPFDL 59
QY 82 KYPLILANGALAAFSIATLRFSIDPLRSLYAEGFVKTLCSYCN-PTDVAATWSFAPALS 140
Db 60 TGPLNLNAGLAIFSTGLSLATTFGLLHEFFRGRGFESYIHIGDFYNGLSGHTWLFVLS 119
QY 141 KIVELGDTWFIILRKRLPIFLHYHAAVLIYTVHSGAETHRAGRFLIMNYFAHSLMYT 200
Db 120 KYAEFGDTLFIILRKRLPIFLHYHAAVLIYTVHSGAETHRAGRFLIMNYFAHSLMYT 179
QY 201 YTVSANGYELPKVWSMTVTQTTOMLAGVITWYKVKTEYKLPQOOSVAN-----LY 256
Db 180 TYMLRSFGVKVPFAWIAKNTITWQILQFV---ITHPIL-FHVGYLAVTQOSVDSTEGYTW 234
QY 257 LAFVIYVTFPAIFIOFFVKAYIILKSKSKSVK 289
Db 235 FCLLMEISIVVLFQNPYYQSYIKGGGKKFNAEK 267

RESULT 5
T22789
hypothetical protein P56H11.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C;Accession: T22789
R;Wilkinson, J.
submitted to the EMBL Data Library, January 1996
A;Reference number: Z19616
A;Accession: T22789
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-288 <WIL>
A;Cross-references: EMBL:Z68749; PIDN:CAA92958.1; GSPDB:GN00022; CESP:P56H11.4
A;Experimental source: clone P56H11
C;Genetics:
A;Gene: CESP:P56H11.4
A;Map position: 4
A;Introns: 49/3; 110/1; 238/3
C;Superfamily: Saccharomyces probable membrane protein YCR034w

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Query Match      23.3%; Score 360; DB 2; Length 288;
Best local Similarity 31.3%; Pred. No. 2.9e-24;
Matches 76; Conservative 58; Mismatches 107; Indels 2; Gaps 2;

QY      48 FQKYVHSISIVLYFILIKVIOKFMENRKPFETLKYPILILWNGALAAFSIIATLRFSDIP 107
      Db      40 FADHFDVTIQASILYGVVVFCTKWFMENRQPFQLTIPLNIWNFIILAAFSIAGAVKMTPEF 99

QY      108 LRSIYASGYFTKLYCSCNPT-DVAAFWSPAFALSKIIVELGDTMFIIILKRPLIELHYVHH 166
      Db      100 FGTIANKGIVASVYCKVDFDPTKGENGYVWVLFMASKLFDLVDTIFLVLKRKGLPLMLPLHYVHH 159

QY      167 AAVLIIVYVHSGAETHAAGRFYILMNLYFAHSLIMNYTYTVSVMGYRLPKWVSMVTVTVTQTQ 226
      Db      160 ILTFVIYAWYSHPLTEGFNRYGIYLVFVVFHAPMYSYVFLRSMKIRVPGPIAQAITSLSQIVQ 219

QY      227 MLAGVGITVMVYKVKRYEKLPCQOSVANLYLAFVIYVTFALLTFQFFVKAYIIKSSK-KS 285
      Db      220 FIFSCAVLAHLGYLMHMTNANCDPEPSVFKLAVFMDITYLALFVNFQLQSVYLRGGDKY 279

QY      286 KSV 288
      Db      280 KAV 282

RESULT 6
T22791
hypothetical protein F56H11.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T22791
R;Wilkinson, J
Submitted to the EMBL Data Library, January 1996
A;Reference number: Z19616
A;Accession: T22791
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-281 <WIL>
A;Cross-references: EMBL;Z68749; PIDN:CAA92960.1; GSPDB:GNO0022; CESP:F56H11.3
A;Experimental source: clone F56H11
C;Genetics:
A;Gene: CESP:F56H11.3
A;Map position: 4
A;Introns: 71/3; 132/1; 178/2; 215/2; 266/2

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Query Match      21.3%; Score 329; DB 2; Length 281;
Best Local Similarity 31.7%; Pred. No. 1.5e-21;
Matches 77; Conservative 49; Mismatches 93; Indels 24; Gaps
7;

Qy 42 QYWTIL-----FQRYWYHSITISVLVYFILIKVIOKFMENRKPFTLKYP LI 86
Db 41 ELSSLNTQDEVFPHISARRFIQEHGFLVQMAJAYVILVPSIKRFMRDREFFQLTALR 100
Qy 87 LWNGLAANFSIIAT---LRPSIDPLRSIYABGFYKTLICYS-CNPTDVAANFWSFAPALSKI 142
Db 101 LWNPFLLSVFSYGSWTWPPFVQOIR-LY--GLGCGCGEALSNLPSQABYWLFIUTILSKA 157
Qy 143 VELGCTWFILRLKRKPLIFLHYTHAAVLIIYVTHSGAEHTAAGRFYILMNYFAHSLMITYY 202
Db 158 VEFVDTFFVLRLKKPLIFLHWYHEMATVFPVFCNSQSRVGVIVNLVFVHAFMYPY 217
Qy 203 TVSANGVELPKVGSMTVTYVTTQTTQCLAGV-GITWVYKVKI-EYKLPQQQSVAANLYLAFV 260
Db 218 FTRSNLKVPAKISMAVTLVQLTQFMCFIYQCTLMYSLATNQARYSNTPATLQCLSYT 277

Qy 261 IYV 263
Db 278 LHL 280

```

RESULT 7
E88690
protein F4IH10.7 [imported] - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: E38690
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology
A;Reference number: A75000; MUID:99049613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.el
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an
A;Accession: E38690
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-286 <SPO>
A;Cross-references: GB:chr_IV; PIDN:AB031174.1; PID:G1397335; GSPDB:GN00022; CESP:F41H1
C;Genetics:
A;Gene: F41H10.7
A;Map position: 4

Query Match	21.2%	Score	327.5;	DB 2;	Length	286;			
Best Local Similarity	32.8%;	Pred.	No. 2.1e-21;						
Matches	80;	Conservative	44;	Mismatches	109;	Indels	11;	Gaps	16;
QY	55	SITISVLYFIILKVIQIFMENRKFPTIKYPLLIWNGALAAFSIIATIRPSIDPLRS-LYA	113						
Db	38	SAKLAVGYIATIGLKYVMKDKAFDLSFTELNIWNGILSTFSLGLFL-FTFPTLLSVIRK	96						
QY	114	BGPYKTLCY--SCNPDTVAAPNSFAFALKIVELGDMPIILKRPLIFLVYVHRAVL	171						
Db	97	DGSHTYSHVSELYTOSTSGYIWFILWISKIPELDTPFVILRKRPUIFMGHWHHAUTG	156						
QY	172	YTV---HSGAEHTAAGRFPILMNYFPAHSLMYTYTYSAMGYRLPKWMSMTVTQTQML	228						
Db	157	YALVCYHEDAVHMV---VVWMYNYIIHAPMGYYLLKSLKVPVPPSVAQAITYSQMWQFA	213						
QY	229	AGV-GITWVYVKYTEVLCPCQOSVANLYLAFVIYVFTEAILPFOFPKVAYIIKSSKS	287						
Db	214	VAlPAQHVSXKHVVEGEVLASFPGTAIGFPMLTIFYFLWLQFYKEHYLKNKGKKYNL	273						
QY	288	VONE	291						
Db	274	AKQD	277						

RESULT 8
T37734
SUR4 family protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000
C:Accession: T37734; T33101
R:Wedler, H.; Duesterhoef, A.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1999
A:Reference number: Z21742
A:Accession: T37734
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-328 <WED>
A:Cross-references: EMBL:AL117213; PIDN:CA355289.1; GSPDB:GN00065; SPDB:SPAC1639.01c
A:Experimental source: strain 972h-; cosmid cl639
R:Wedler, H.; Duesterhoef, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1999
A:Reference number: Z21827
A:Accession: T39101
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-328 <WE2>
A:Cross-references: EMBL:AL117212; PIDN:CA355288.1; GSPDB:GN00065; SPDB:SPAC806.09c
A:Experimental source: strain 972h-; cosmid c806
C:Genetics:
A:Gene: SPAC806.09c; SPAC1639.01c
A:Map position: 1
A:Introns: 5/2; 125/3
C:Superfamily: Saccharomyces probable membrane protein YCR034w

A;Gene: SGD:SURA; SRE1; APAL
A;Cross-references: SGD:S0004364; MIPS:YLR372w
A;Map position: 12R
C;Superfamily: Saccharomyces probable membrane protein YCR034w
C;Keywords: transmembrane protein
F;69-89/Domain: transmembrane #status predicted <TM1>
F;110-129/Domain: transmembrane #status predicted <TM2>
F;148-166/Domain: transmembrane #status predicted <TM3>
F;209-229/Domain: transmembrane #status predicted <TM4>
F;243-263/Domain: transmembrane #status predicted <TM5>
F;283-304/Domain: transmembrane #status predicted <TM6>

Query Match 17.0%; Score 262; DB 2; Length 345;
Best Local Similarity 28.9%; Pred. No. 1.5e-15;
Matches 82; Conservative 53; Mismatches 115; Indels 34; Gaps 11;

QY 27 YKYSHPGEQVADPYQTIIIFQKYVHSITISVLVFIILIKVIQKME--NRKEPTLKYP 84
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 50 FEYFGSPAEQPEFHINKTFLAN--GYHVGSIIVVIIIFGGOAILFALNASLTKLL 107
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 85 LILWNGAAASLIATLRFSDPLSLYAEGFYKLC--YSCNPDTDVAAPWSFAFALSKI 142
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 108 FEIHLFTLSLVLMMLBQLPVMVYHNLFSICSKAFAPKLVTLY--YLNYLTKP 165
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 143 VELGDTFMIIIRKRPIELFHYTH--AAVLITYVHSGAEHTAAGRPXYILMYFAHSLMYT 200
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 166 VELIDTVFLVRKKLLFLHYHGATALLCYTLIG--RTSVEMVVILLNLGVHVIMYW 223
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 201 YTVTSANGRYLPKWMSMTVTVTOTMLAGVGTIMVVKTEY-----KLPCQ 249
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 224 YYFLSSCGIRV--NWKQWTRFQIIQFL--IDLVFVFATVIFYAHKYLDGILPNKGTCY 279
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 250 QSVANLYLAFLVYVTFAILFIQFFKVAYIKSSKK--SKSVKNE 291
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 280 GTQAAAAGYLLNSYLLLFISFVIQS-----KKGKKTKVKE 318
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 10
T50139
GN31/SUR4 family protein [imported] - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
C;Accession: T50139
R;Barrell, B.G.; Rajandream, M.A.; McDougall, R.C.
submitted to the EMBL Data Library, November 1999
A;Reference number: Z25042
A;Accession: T50139
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-334 <BAR>
A;Cross-references: EMBL:AL3157; PIN: CAB61470.1; GSPDB: GN00066; SPDB: SPAC1B2.03c
A;Experimental source: strain 972h(-); cosmid c1B2
C;Genetics:
A;Gene: SPDB:SPAC1B2.03c
A;Map position: 1
A;Introns: 25/2
C;Superfamily: Saccharomyces probable membrane protein YCR034w

Query Match 15.2%; Score 235.5; DB 2; Length 334;
Best Local Similarity 28.2%; Pred. No. 3.1e-13;
Matches 71; Conservative 50; Mismatches 102; Indels 29; Gaps 9;

QY 53 YHSITIISV-LYFILIKVIQKMEKRP-----FTL-KYPLLNGALAAEFSIATLRPS 104
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 55 WSSVITSVTAYVILSGLRAMTRNKPKQRRLPOLNFILTIISGALLLV----- 107
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 105 IDPLRSYAEGFYKTYCVSCNPDTDVAAPWSFAFALSRIVELGDTFMIIIRKRPIELFHY 164
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 108 EEVFENYMENGLFYVCVDSRHFTQRLVTLVLYNLTKYLELMDTVFLFKKKPLAFHCY 167
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 165 HH--AAVLITYVHSGAEHTAAGRPXYILMYFAHSLMYTIVTSANGVRLPKWMSMTVTY 222
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 168 HHGITALLCTQLLGRTSVQNG--VIGLNLYVHMVTSYYFLAACGRRV--WFKQWTRV 223
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 223 OTTOMLAGVITWYKTEYK-----LP-----COOSVANLYLAFVIYVTFAILFIQFFV 274
 DB 224 QIIQFVLDLILCYFTGYSHIAFRPPWLPVHVDGSGSLFAFFGCVLSSVLFPIGFYI 283
 QY 275 KAYIIKSKKKK 286
 DB 284 NTYIKRGAKNQ 295

RESULT 11

S46638
 Probable membrane protein YCR034w homolog YJL196c - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein 00343; protein YJL196c
 C:Species: Saccharomyces cerevisiae
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
 A:Accession: S46638; S56983
 R:Purnelle, B.; Coster, F.; Goffeau, A.
 Yeast 10, 1235-1249, 1994
 A:Title: The sequence of a 36 kb segment on the left arm of yeast chromosome X identifies
 a gene ACO1 and two homologues to chromosome III genes.
 A:Reference number: S46621; MUID:95274326; PMID:7754713
 A:Accession: S46638
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-310 <PUW>
 A:Cross-references: EMBL:X77688; NID:gl183992; PIDN:CAA54764.1; MIPS:YS47599
 R:Purnelle, B.; Coster, F.; Goffeau, A.
 submitted to the Protein Sequence Database, September 1995
 A:Reference number: S56977
 A:Accession: S56983
 A:Molecule type: DNA
 A:Residues: 1-310 <PUW>
 A:Cross-references: EMBL:249471; NID:gl008410; PID:gl008411; MIPS:YJL196c
 C:Genetics:
 A:Gene: SGD:ELO1
 A:Cross-references: SGD:S0003732; MIPS:YJL196c
 A:Map position: 101
 C:Superfamily: Saccharomyces probable membrane protein YCR034w
 C:Keywords: transmembrane protein

Query Match 14.3%; Score 220.5; DB 2; Length 310;
 Best Local Similarity 27.0%; Pred. No. 5.9e-12;
 Matches 66; Conservative 48; Mismatches 111; Indels 19; Gaps 7;
 QY 61 LYELIKVIQFMENRKPFTLKYPILLWNGALAFSIIATIRPSIDPLRSIYAGFYKTL 120
 DB 71 MYVVIFGGRSLVSKCKPLKRFISQVHNLMLTSSVFLMLIYVEQMLPIVYRHGLYFV 130
 QY 121 CYS---CNPTDVAAPFWSFAFALSXIVELGDTMFIILKRPLIPFLHYHHAVALIYTVHSG 177
 DB 131 CNVESWTQPMETLYLNY--MTKVFEPADTVLVLKHKRLTFLHTYHGGATALLCYNQL 187
 QY 178 AEHTAAGRFYILMNYFAHSLMYTYTVVSAMGYRLPKWVSMVTVTQTQ-MLAGVGTWM 236
 DB 188 VGYTAVTVVPVTLNLAHVLMVYFSLASGIRV--WKAWVTFRQIIQFVLDIGFIYPAVY 245
 QY 237 VYK--VKTEYKLPQOQ-----SVANLYLAFVIYVTFAILFIQFFVKAVIILKS-SKSK 286
 DB 246 LYQKIVAAFYKNACTPQCEDCLGSMATAAGAAITLSYLFPIGFYIEVYKRGASGKK 305
 QY 287 SVKN 290
 DB 306 INKN 309

RESULT 12

S12916
 Probable membrane protein YCR034w - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein YCR521
 C:Species: Saccharomyces cerevisiae
 C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 21-Jul-2000
 A:Accession: S12916; S40919; S19446

R;Thierry, A.; Fairhead, C.; Dujon, B.
 Yeast 6, 521-534, 1990
 A:Title: The complete sequence of the 8.2 kb segment left of MAT on chromosome III reveals
 A:Reference number: S12916; MUID:91181345; PMID:1964349
 A:Accession: S12916
 A:Molecule type: DNA
 A:Residues: 1-347 <THI>
 A:Cross-references: EMBL:X56909; NID:g4489; PIDN:CAA40226.1; PID:g4490
 R;Wicksteed, B.L.; Roberts, A.B.; Sagliocco, F.A.; Brown, A.J.P.
 Yeast 7, 761-772, 1991
 A:Title: The complete sequence of a 7.5 kb region of chromosome III from Saccharomyces
 A:Reference number: S40917; MUID:92133166; PMID:1776366
 A:Accession: S40919
 A:Molecule type: DNA
 A:Residues: 1-347 <WIC>
 A:Cross-references: EMBL:S78624; NID:g244237; PIDN:AAB21360.1; PID:g244240
 R;Dujon, B.; Fairhead, C.; Thierry, A.
 submitted to the Protein Sequence Database, March 1992
 A:Reference number: S19446
 A:Accession: S19446
 A:Molecule type: DNA
 A:Residues: 1-347 <DUJ>
 A:Cross-references: EMBL:X59720; NID:gl907116; PID:gl907176; MIPS:YCR034w
 C:Genetics:
 A:Gene: SGD:FEN1
 A:Cross-references: SGD:S0000630; MIPS:YCR034w
 A:Map position: 3R
 C:Superfamily: Saccharomyces probable membrane protein YCR034w
 C:Keywords: transmembrane protein
 P:67-84/Domain: transmembrane #status predicted <TM1>
 P:110-129/Domain: transmembrane #status predicted <TM2>
 P:151-169/Domain: transmembrane #status predicted <TM3>
 P:198-214/Domain: transmembrane #status predicted <TM4>
 P:236-254/Domain: transmembrane #status predicted <TM5>
 P:275-299/Domain: transmembrane #status predicted <TM6>

Query Match 14.2%; Score 220; DB 2; Length 347;
 Best Local Similarity 28.2%; Pred. No. 7.4e-12;
 Matches 67; Conservative 36; Mismatches 121; Indels 14; Gaps 5;
 QY 62 YFILIYVQFMENRKPFTLKYPILLWNGALAFSIIATIRPSIDPLRSIYAGFYKTL 121
 DB 78 YVYVIFGGRFLSKSPFKLGLFQLHNLVLTSLSLTLLLMVEQLVPIIVQHGLYPAIC 137
 QY 122 YSCNPTDVAAPFWSFAFALSXIVELGDTMFIILKRPLIPFLHYHH--AAVLIYVHSGAE 179
 DB 138 NIGANTQPLVTLVYMYVIVKPIFIDTFVLVLRKKLTFLHTYHGGATALLCYTLMGT- 196
 QY 180 HTAAGRFYILMNYFAHSLMYTYTVVSAMGYRLPKWVSMVTVTQTQMLAGVG-ITWVY 238
 DB 197 -TSISWVPISLNLGVHVMYVYFLAARGIRV--WKKEWTRFQIIQFVLDIGFIYPAVY 253
 QY 239 KVTEYKLP-----COOSVANLYLAFVIYVTFAILFIQFFVKAVIILKS-KSKSKV 289
 DB 254 QKAVHLYFPIPHCGDCVGTATFAGCATISSYLVLFISFYINVKRKGTKTSRVVK 311

RESULT 13

T46257
 Hypothetical protein DKFZp7610031.1 - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 03-Nov-2000
 C:Accession: T46257
 R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, January 2000
 A:Reference number: 223031
 A:Accession: T46257
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-158 <AAA>
 A:Cross-references: EMBL:AL137506
 A:Experimental source: adult amygdala; clone DKFZp7610031
 C:Genetics:

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2004, 15:24:53 ; Search time 45 Seconds
(without alignments)
2040.351 Million cell updates/sec

Title: US-09-936-845A-15
Perfect score: 1545
Sequence: 1 MELAEFNDLNTFTYIGPNH.....PFVKAYIIKSKKSKSVNE 291

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.25:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_virus:
16: sp_bacteriaph:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	659.5	42.7	286	5 Q9NAC6	Q9nac6 caenorhabdi
2	484.5	31.4	316	5 Q9VVR87	Q9vvr87 drosophila
3	447.5	29.0	267	11 Q92015	Q92015 mus musculu
4	447	268	13 Q802X6		Q802x6 brachydanio
5	446.5	28.9	267	11 Q92016	Q92016 rattus norv
6	439.5	28.4	267	11 Q8C245	Q8c245 mus musculu
7	435.5	28.2	265	4 Q9H5J4	Q9h5j4 homo sapien
8	434.5	28.1	240	4 Q9NC01	Q9nc01 homo sapien
9	398	25.8	274	5 Q9XVQ9	Q9xvq9 caenorhabdi
10	396.5	25.7	323	5 Q86LT1	Q86lt1 cryptospori
11	374	24.2	274	5 Q920303	Q920303 caenorhabdi
12	368	23.8	301	5 Q9GNX9	Q9gnx9 leishmania
13	360	23.3	288	5 Q20901	Q20901 caenorhabdi
14	329	21.3	281	5 Q20904	Q20904 caenorhabdi
15	327.5	21.2	286	5 Q20300	Q20300 caenorhabdi
16	323.5	20.9	296	5 Q86JM5	Q86jm5 dictyosteli

17	315	20.4	322	5 Q8I251	Q8i251 plasmodium
18	286.5	18.5	342	13 Q7ZXJ4	Q7zxj4 xenopus lae
19	285.5	18.5	612	5 Q8I2V3	Q8i2v3 plasmodium
20	281.5	18.2	328	3 Q8UR34	Q8ur34 schizosacch
21	276.5	17.9	372	5 Q9BLR0	Q9blr0 leishmania
22	275.5	17.8	282	13 Q7ZTU5	Q7ztu5 brachydanio
23	270.5	17.5	257	5 Q86HP4	Q86hp4 dictyosteli
24	266.5	17.2	329	5 Q8MS02	Q8ms02 drosophila
25	266.5	17.2	365	5 Q8IPL8	Q8ipl8 drosophila
26	265.5	17.2	329	5 Q3VHX7	Q3vhx7 drosophila
27	263.5	17.1	320	13 Q7ZUC3	Q7zuc3 brachydanio
28	263	17.0	364	5 Q9VN29	Q9vn29 drosophila
29	262.5	17.0	312	11 Q8JZV3	Q8jzv3 mus musculu
30	262	17.0	290	13 Q8AVG1	Q8avg1 xenopus lae
31	257.5	16.7	290	13 Q7SY74	Q7sy74 xenopus lae
32	256.5	16.6	288	13 Q7ZVN0	Q7zvn0 brachydanio
33	254.5	16.5	261	5 Q9VH56	Q9vh56 drosophila
34	254.5	16.5	281	11 Q8BYV8	Q8byv8 mus musculu
35	252	16.3	261	12 Q9J5P5	Q9j5f5 fowlpox vir
36	250.5	16.2	281	11 Q9DXF9	Q9dxz9 mus musculu
37	242.5	15.7	281	11 Q8BX38	Q8bx38 mus musculu
38	240	15.5	400	5 Q9GNX8	Q9gnx8 leishmania
39	239.5	15.5	375	5 Q9BLQ9	Q9blq9 leishmania
40	239	15.5	265	5 Q9VH59	Q9vh59 drosophila
41	239	15.5	277	5 Q9VC20	Q9vcz0 drosophila
42	237	15.3	279	4 Q8MXU3	Q8mxu3 homo sapien
43	236.5	15.3	337	3 Q87I85	Q87i85 neurospora
44	235.5	15.2	334	3 Q9UTF7	Q9utf7 schizosacch
45	233.5	15.1	284	5 Q9BLQ8	Q9blq8 leishmania

ALIGNMENTS

RESULT 1

Q9NAC6 ID Q9NAC6 PRELIMINARY; PRT; 286 AA.
AC Q9NAC6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Y53F4B.2 protein.
GN Y53F4B.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
CX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Smye R.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; AL132949; CAB61069.1; --
DR WormPep; Y53F4B.2; CE22398.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR002076; GNSI_SUR4.
DR Pfam; PF01151; ELO; 1.
DR PROSITE; PS01188; ELO; 1.
SQ SEQUENCE 286 AA; 33402 MW; DF9DB8D3B2F1C479 CRC64;

Query Match 42.7%; Score 659.5; DB 5; Length 286;

Best Local Similarity 45.1%; Pred. No. 2.4e-50;

Matches 130; Conservative 51; Mismatches 88; Indels 19; Gaps 3;

Qy 2 ELAEFNDLNTFTYIGPNHDTMTTKYKSYHFFGQVADPQYWTIL-----FQKXYTHSI 56

Db 7 ERFKVMTGNVETIISPFYDSTLLIE-----SWDDLTMTHTFFKNNHFKSV 53

QY 57 TISVLVIFILKVIQKFMENRPFILKVIPLIWLNGALAAFSIIATLRFSIDPLRLSYAEGF 116
 DB 54 YLSAAYFIATNLQRYMESRDKPMRPLLLAWNGFLAVFSGTWRFGEIYDAVFRGF 113
 QY 117 YKTLTCSNCPDVAAFNSFAFALSKIVELGDTMFIILKRPLIFLHYHHAALVITYVHS 176
 DB 114 IDSICLVNPRSPSAFWACMFALSKIAEFGDTMFLVLRKRPVIFLHYHHAALVILSWHA 173
 QY 177 GABHTAAGRFVILKYNFANSLMYTYTVSANGYPLPKWMSMTVTVTQOTLQAGVITWM 236
 DB 174 AIELTAPGRWIFKNYLVHSMYTYTATISGYLPRKIVSMVTFLQTLQMLGVISICI 233
 QY 237 VYKVKTEYKLPQOOSVANLYAFIYVTFALLFIQFFVXVILKSSKK 284
 DB 234 VLXLKNGEM-CQSYDNLALSPGIYASFLVLFSSFNNAVYVKDKKK 280

RESULT 2
 Q9VV87
 ID Q9VV87 PRELIMINARY; PRT; 316 AA.
 AC
 DT Q9VV87; Q9NB55;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE CG3971 protein (putative multipass transmembrane) (Transmembrane
 protein Noa) (L010431p)
 GN BALDSPOT OR NOA OR CG3971.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Prexygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN (1)
 R2 SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S.E., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Shandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos A., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinart K., Remington X., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svizkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.N., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";
 Science 287:2185-2195 (2000).

[2]

SEQUENCE FROM N.A.

RA Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Ananides P.G., Brandon P.C., Rogers Y.,
 RA Banon J., An H., Baldwin D., Beeson K.Y., Beeson L.B., Dietz S.M.,
 RA Carlson J.W., Center A., Champagne M., Davenport L.B., Farfan D.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferrera S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gezagale M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacleb J., Paragab V., Park S., Patel S., Pfeiffer B., Scheeler F.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svizkas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of Drosophila melanogaster genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]

SEQUENCE FROM N.A.

RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris M.,
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smurniak P., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of Drosophila melanogaster genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]

SEQUENCE FROM N.A.

RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]

SEQUENCE FROM N.A.

RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]

SEQUENCE FROM N.A.

RA Rice A.H., Page C., Duffy J.B.;
 RT "Sequence analysis and characterization of baldpot.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]

SEQUENCE FROM N.A.

RA Jung A.G., Schaefer M.A.;
 RT "The noa gene encodes a member of a widely distributed family of
 integral membrane proteins in Drosophila";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [8]

SEQUENCE FROM N.A.

RA STRAIN=Berkley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champagne M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarini H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacleb J., Paragab V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF003526; AAF49430.2; -
 DR EMBL; AF265296; AAF75771.1; -
 DR EMBL; AF279258; AAG02080.1; -
 DR EMBL; AF279257; AAG02080.1; JOINED.
 DR EMBL; AY061121; AAL28669.1; -
 DR FlyBase; FBgn003650; Baldepot.

DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR002076; GNS1 SUR4.
 DR InterPro; IPR005806; Rieske_dom.

DR Pfam; PF01151; ELO; 1.
 DR PROSITE; PS01188; ELO; 1.
 DR Transmembrane.
 SQ SEQUENCE 316 AA; 36829 MW; E741960F28D2A3AD CRC64;

Query Match 31.4%; Score 484.5; DB 5; Length 316;
 Best Local Similarity 37.7%; Pred. No. 7.9e-35;
 Matches 103; Conservative 54; Mismatches 99; Indels 17; Gaps 5;

QY 23 MTKYKSYHFGGEVADP-----QYTWLFOKWYHSITISVLYFLIKVKQFMR 76
 DB 8 VTPNYSYIFDENDHRTKMLLENWTWF---YYCGI-----YMLVFGGQHFQNR 59

QY 77 KPFTLKYPILWNGALAAFSIATIRFSDIPRSIYAEFGYKTLCS--CNFTDVAAPWS 134
 DB 60 PRFQLRGFLIIWNTLLANFSINGARTAPELLHVLHVGPHSVCPYSYISQDRVCGFWT 119

QY 135 FAFALSKIVELGDTWFIILRRPLIFLHYHAAVLIYTVHSGAEHTAAGRFYILMYFA 194
 DB 120 WLFVLSKLPGLGDTFIFVLRKQPLIFLHYHHTVLIYSWFSYTEYTSARAFWIMYCV 179

QY 195 HSLMYTYTVSANGYRLPKWSMTVTVTQTMLAGVCI-TWVYKVKTEYKLPQQQSV 253
 DB 180 HSNVYSYALKAAEPNPRFISMITSQLAQMIIGCAINWANGFLKTHGTSSCHISQR 239

QY 254 NLYLAFLVYVTFALFIOFFVKAYIIKSSKSK 286
 DB 240 NINLSIAMYSYFVLFARFFYKAVLAPGCHSKR 272

RESULT 3

Q920L5 PRELIMINARY; PRT; 267 AA.

AC Q920L5; (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 25, Last annotation update)
 DE Fatty acyl elongase (Long-chain fatty-acyl elongase) (Myelination associated SUR4-like protein).
 GN ELOVL6 OR FAE OR ICE OR XASR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=CS7B16; TISSUE=Liver;
 RA Matsuzaka T., Shimano H.;
 RT "murine complete cds for new fatty acyl elongase similar to cig30 (U97107).";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21576178; PubMed=11567032;
 RA Moon Y.A., Shah N.A., Mohapatra S., Warrington J.A., Horton J.D.;
 RT "Identification of a Mammalian Long Chain Fatty Acyl Elongase Regulated by Sterol Regulatory Element-Binding Proteins.";
 RL J. Biol. Chem. 276:45339-45366 (2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Nagarajan R., Le N.H., Mahoney H., Azaki T., Milbrandt J.D.;
 RT "Deciphering Peripheral Nerve Myelination Using Schwann Cell Expression Profiling";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 EN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZSCH 11; TISSUE=Breast tumor;
 RA Strausberg R.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB072039; BAB68544.1; -
 DR EMBL; AF053453; AALJ4239.1; -
 DR EMBL; AF480860; AAMJ3450.1; -
 DR EMBL; BC051041; AAH51041.1; -
 DR MGD; MGI:2156528; Elovic6.
 DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; IDA.
 DR GO; GO:0016747; P:transferase activity, transferring groups o...; IDA.
 DR GO; GO:0030497; P:fatty acid elongation; IDA.

DR InterPro; IPR002076; GNSI_SUR4.
 DR Pfam; PF01151; ELO; 1.
 DR PROSITE; PS01188; ELO; 1.
 SQ SEQUENCE 267 AA; 31610 MW; 4026C9C33FDD023 CRC64;

Query Match 29.0%; Score 447.5; DB 11; Length 267;
 Best Local Similarity 36.9%; Pred. No. 1.2e-31;
 Matches 97; Conservative 50; Mismatches 109; Indels 7; Gaps 3;

QY 26 KYKYSVHPGGEVADPQYTWLFOKWYHSITISVLYFLIKVKQFMRKPFTLKVPL 85
 DB 10 EYEFKQFNEVAIQ---W---MQENWKKSFLFSALYAAFPGRHLMKRAKPELRKPL 63

QY 86 ILWNGALAAFSIATIRFSDIPRSIYAEFGYKTLCS--CNFTDVAAPWSAFALSKIVE 144
 DB 64 VLASLTAVFSIFCALRTGAYMLYILMTKLGKQSCVDCQSFYNGPVSXFWAYAFVLSK 123

QY 145 LGDTMFIILRRPLIFLHYHAAVLIYTVHSGAEHTAAGRFYILMYFAHSLMYTYTV 204
 DB 124 LGDTFIIILRRKQLIFLHYHHTVLIYSWYKQVAGGGMFTWYGVHVMYSIAL 183

QY 205 SAMGYRLPKWSMTVTVTQTMLAGVCI-TWVYKVKTEYKLPQQQSVANLYLAFLVYV 264
 DB 184 RAAGFVSRKFAFITLSQITQMLGCVINLYVFNWQHDNDCCYSHFQIFWSSLMYLS 243

QY 265 FALFIOFFVKAYIIKSSKSKS 287
 DB 244 YLVLFCHFFFEYIGYKVKATKA 266

RESULT 4

Q802X6 PRELIMINARY; PRT; 268 AA.

AC Q802X6; (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Similar to fatty acid elongase 2.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
 NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC046901; AAH46901.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR InterPro; IPR002076; GNSI_SUR4.
 DR Pfam; PF01151; ELO; 1.
 DR PROSITE; PS01188; ELO; 1.
 SQ SEQUENCE 268 AA; 31386 MW; CDD41ACAL1639928 CRC64;

Query Match 28.9%; Score 447; DB 13; Length 268;
 Best Local Similarity 36.2%; Pred. No. 1.4e-31;
 Matches 101; Conservative 60; Mismatches 100; Indels 18; Gaps 8;

QY 19 NHTDM---TTKYKSYHFGGEVADPQYTWLFOKWYHSITISVLYFLIKVKQFMR 75
 DB 2 NMTDFQLPTEYEFERHF-DERLAIE--W---MQDNWKKSFPGAVTVLVFGQHFQMD 55

QY 76 RKPFLLKYPILWNGALAAFSIATIRFSDIPRSIYAEFGYKTLCS--CNFTDVAAP 132
 DB 56 QRDLRLKVLMMWSLSLAIFSIIICAVRTGCFMLYILSTSGFKQSCVDCQSFYNGP--ISK 113

QY 133 WSEFALSKIVELGDTWFIILRRPLIFLHYHAAVLIYTVHSGAEHTAAGRFYILMY 192
 DB 114 WACAFVLSKAPGLGDTMFIILRRKQPLIFLHYHHTVLIYSWFSYTEYTSARAFW 173

QY 193 FAHSLMYTYTVSANGYRLPKWSMTVTVTQTMLAGVCI-TWVYKVKTEYKLPQQQSV 252
 DB 174 TVHALMYSYAAARAAGLRVFKPCAILITSQIAQAMDLAVSLVYRWMDG--DCFSYL 231


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KW Hypothetical protein.
SQ SEQUENCE 265 AA; 31376 MW; 01234E0BEF6CE341 CRC64;

Query Match      28.2%; Score 435.5; DB 4; Length 265;
Best Local Similarity 35.8%; Pred. No. 1.4e-30;
Matches 95; Conservative 54; Mismatches 103; Indels 13; Gaps 5;

QY 26 KYKSYHPPGQGVADPOYTWILFQKYWHSTISVLYFILIYKVIQKFMENKPFLLKPYL 85
DB 10 EYEFKQFNEAIQ---W---MQENWKSGFLFSALYAAFIQGRHLNKRKAFELRKPL 63

QY 86 ILNMGALAAFSIIATLRFSDPLSLYAGFYKTLCL---YSCNPTDYAAFWAFAPALSKI 142
DB 64 VLSLTLAVSFICALTGTGAWYILMTKGLKQSVCDQGFYNGP--VSKFWAYAFVLSKA 121

QY 143 VELGDTMFIILRKLPLFLHYHAAVLIYVHSGAEHTAAGRFYILMNYFAHSLMYTYV 202
DB 122 PELGDTIPIILRKQKLIHLHWHHTVLLYLSWYSYKDMVAGGCFWMTMNVGVHAWYSY 181

QY 203 TVSAMGVLPKWSMTVTVTQTMKLAGVITWMVYKVTYKLPQOOSVANLYLAFVIY 262
DB 182 ALRAAGFRVSRKFAFMTISQITQMLMGCVVNYLVFCWMQHDQ--CHSHFQNIWFWSLMY 239

QY 263 VTFAILFIQPFVKAYIIKSKSKS 287
DB 240 LSVLVLPCHFPPEAYIGKMKTKA 264

RESULT 8
Q8NCD1
ID Q8NCD1 PRELIMINARY; PRT; 240 AA.
AC Q8NCD1;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Hypothetical protein FL390332.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Masuho Y., Oho T., Okano K., Yoshikawa Y., Iotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT "NEO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK074813; BAC11225.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR002076; GNS1_SUR4.
DR Pfam; PF01151; ELO; 1.
DR PROSITE; PS01188; ELO; 1.
KW Hypothetical protein.
SQ SEQUENCE 240 AA; 28271 MW; 38A101DCFT41818E CRC64;

Query Match      28.1%; Score 434.5; DB 4; Length 240;
Best Local Similarity 38.0%; Pred. No. 1.6e-30;
Matches 92; Conservative 50; Mismatches 93; Indels 7; Gaps 3;

QY 49 QKWWHSITISVLYFILIYKVIQKFMENKPFLLKPYLILNMGALAAFSIIATLRFSDPL 108
DB 2 Q8NWKSFSLYAAFIQGRHLNKRKAFELRKPLVLSLTLAVFSIFGALRTGAYMV 61

QY 109 RSLYAGFGFYKTLCL---YSCNPTDYAAFWAFAPALSKIIVELGDTMFIILRKLPLFLHYH 165
DB 62 YILMTKGLKQSVCDQGFYNGP--VSKFWAYAFVLSKAPELGDTIPIILRKQKLIHLHWH 119

QY 166 HAAVLIYVHSGAEHTAAGRFYILMNYFAHSLMYTYVTVSAMGVLPKWSMTVTVTQTT 225
DB 120 HITVLLYSYKDMVAGGCFWMTMNVGVHAWYSYALRAAGFRVSRKFAFMTISQIT 179

QY 226 QMLAGVIGITWMVYKVTYKLPQOOSVANLYLAFVIYVTFAILFIQPFVKAYIIKSKSKS 285
DB 180 QMLMGCVVNYLVFCWMQHDQ--CHSHFQNIWFWSLMYLSYLVLPCHFPPEAYIGKMKTK 237

QY 286 KS 287
DB 238 KA 239

RESULT 9
Q9XVQ9
ID Q9XVQ9 PRELIMINARY; PRT; 274 AA.
AC Q9XVQ9;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Fl186.5 protein.
GN Fl186.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Matthews L.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; Pubmed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z81058; CAB02921.1; -.
DR PIR; T20786; T20786.
DR WormPep; Fl186.5; CE19785.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR002076; GNS1_SUR4.
DR Pfam; PF01151; ELO; 1.
DR PROSITE; PS01151; ELO; 1.
SQ SEQUENCE 274 AA; 31361 MW; 2CBB7DASFP418D714 CRC64;

Query Match      25.8%; Score 398; DB 5; Length 274;
Best Local Similarity 37.1%; Pred. No. 3e-27;
Matches 89; Conservative 48; Mismatches 99; Indels 4; Gaps 4;

QY 55 SITTSVLYFILIYKVIQKFMENKPFLLKPYLILNMGALAAFSIIATLRFSDPLSLYAE 114
DB 36 SYKIMIGYLVITYPGQKLAHAKPFDLQNTLALNFGSFLSGIAAYKLIPELFGVPMKD 95

QY 115 GPYKTLGVSCN-PDVA-AFWSPAPALSKIIVELGDTMFIILRKLPLFLHYHAAVLIY 172
DB 96 GFVASVQCNENYTTDASTGFGWAFVMSKAPELGDTMFLVLRKPVIPFWHWHALTFVY 155

QY 173 TVHSGAEHTAAGRFYILMNYFAHSLMYTYVTVSAMGVLPKWSMTVTVTQTMKLAGV 232
DB 156 AVTYSEHQAWARWSLALNLAHVTVMYFYFAVRALNIQTFRPAKFITTIQIVQFVISCY 215

QY 233 ITWMVYKVTYKLP-CQOOSVANLYLAFVIYVTFAILFIQPFVKAYIIKSKSKSVKNE 291
DB 216 IFGHVLIKSDSPGCAVSNVLSIGLMIISYLVLPFAKFFYKAYIQRS-PIKSKQE 274

RESULT 10
Q86LT1
ID Q86LT1 PRELIMINARY; PRT; 323 AA.
AC Q86LT1;
DT 01-JUN-2003 (TREMblrel. 24, Created)
DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Putative fatty-acyl elongase.
GN FAELO1.
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;

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Db 28 FDYFDVLVYSEVLVIVLFLGPKAMESREPRLRLYLIAWNLALSFSLGCTGVSIML 87
QY 108 LRSLYAGSYKTLCSNCPDVA-----AFWSPAFALSKIVELGDTMFILRKRLIFL 161
Db 88 MSLSEERGMYETTCY----LDKSLYDGLTFLFAPFLSKIPMLDTFVLVTKKPIIFL 143
QY 162 HYYHRAVLIVYHSGAHTAGRFVILMNYFAHSLMYTYTYSAMGYR-LPKWYSMTVT 220
Db 144 EYHHLTVTFVCWYAGYTLIAGVAFASWNYAVHVMYFYFLCSLGMKRLIRPIAPT 203
QY 221 TVQTTQMLAGVGITWMVYKTEYLPCCQSVANLYLAFVIYVTFAILFIQFFKAYIIR 280
Db 204 GAQLLQMVVGTIIVLTYFYGYISERGCGVDHRTIRMGLCMYSYFVLFAFLFVRLY-MK 262
QY 281 SSKSKSKVQNE 291
Db 263 KGAVTKSRKTE 273

RESULT 13
Q20901 PRELIMINARY; PRT; 288 AA.
AC Q20901;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-JAN-1998 (TremBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Long chain POLYUNSATURATED fatty acid elongation enzyme.
GN CEELO1 OR F56H11.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Das T., Parker-Barnes J.M., Thurmond J.M., Bobik E., Leonard A.E.,
RA Chuang L., Huang Y.-S., Mukerji P.;
RT "Identification and characterization of novel polynunsaturated fatty
RT acid elongating enzymes from Mortierella alpina and Caenorhabditis
RT elegans."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Wilkinson J.;
RA Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF244356; RAF70462.1; -.
DR EMBL; 268749; CAA92958.1; -.
DR PIR; T22789.
DR WormPep; F56H11.4; CE05979.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR Pfam; PF01151; ELO; 1.
DR PROSITE; PS01188; ELO; 1.
SQ SEQUENCE 288 AA; 33561 MW; 8BA5CD4892012B0E CRC64;

Query Match 23.3%; Score 360; DB 5; Length 288;
Best Local Similarity 31.3%; Pred. No. 7.2e-24;
Matches 76; Conservative 58; Mismatches 107; Indels 2; Gaps 2;

QY 48 FQYVHSTITISVLPIKVIQKFMENRKPFTLKYPLIMNGALAAFSIATLRFSDIP 107
Db 40 FADHPDVTIQASILYMWVFGTKWFRNRQPFQATPLINWFIILAAFSIAGAVMTPEF 99
QY 108 LRSLYAGSYKTLCSNCPET-DVAAPWSPAFALSKIVELGDTMFILRKRLIFLHYHH 166
Db 100 FGTIANKGIVASVCKVDFDTKGNGYVWFLFWASKLFLVDVDFLVRKRPLMLFHWYHH 159
QY 167 AAVLIYVHSGAHTAAGRFVILMNYFAHSLMYTYTYSAMGYR-LPKWYSMTVTVQTTQ 226
Db 160 ILTMIVAWYSHPLTPGFNRYGIVLNFVHAPMYSYFLFSMKIRVPGPIAQAITSLQIVQ 219
QY 227 MLAGVITWMVYKTEYLPCCQSVANLYLAFVIYVTFAILFIQFFKAYIIRKSK-KS 285
Db 220 FIISCAVLAHLGYLMEFTNANCDPESVFKLAVFDVDTYLLALFVNFPLQSYVLRGGDKY 279
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QY 286 KSV 288
Db 280 KAV 282

RESULT 14
Q20904 PRELIMINARY; PRT; 281 AA.
AC Q20904;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE F56H11.3 protein.
GN F56H11.3
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilkinson J.;
RA Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RL EMBL; 268749; CAA92960.1; -.
DR PIR; T22791; T22791.
DR WormPep; F56H11.3; CE16144.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR002076; GNS1_SUR4.
DR Pfam; PF01151; ELO; 1.
DR PROSITE; PS01188; ELO; 1.
SQ SEQUENCE 281 AA; 33441 MW; 825D529D7FEBF936 CRC64;

Query Match 21.3%; Score 329; DB 5; Length 281;
Best Local Similarity 31.7%; Pred. No. 3.9e-21;
Matches 77; Conservative 49; Mismatches 93; Indels 24; Gaps 7;

QY 42 QYWTIL-----FQYVHSTITISVLPIKVIQKFMENRKPFTLKYPLI 86
Db 41 ELSLLTNQDEVPFHIRARRFIQSHFGFLVQMAIAYVILVFSIKRMRDRPFLQTTALR 100
QY 87 LNWGALAAFSIAT---LRFSIDPLRSIYAGFYKTLCSY-CNPTDVAAPWSPAFALSKI 142
Db 101 LWNFSLSVFSYSGSWTFPFVQOIR-LY--GLYCGCEALSNLPSQAEYVNLFLTILSKA 157
QY 143 VELGDTMFILRKRLIFLHYHHAALVIVYHSGAHTAAGRFVILMNYFAHSLMYTY 202
Db 158 VEFVDTFPLVLRKKFLIFLHWYHMAITFVFPSCSYPTPSSQSRVGVIVNLVFWHAPMYPY 217
QY 203 TVSANGVELPKWYSMTVTVQTTQMLAGV-GITWVYKVKT-EYKLPCCQSVANLYLAFV 260
Db 218 FTRSNWIKVPKISMAVTVLQDTQFNCFIYGTCLMYSLATNQARYPSNTATLQCLSYT 277
QY 261 IYV 263
Db 278 LHL 280

RESULT 15
Q20300 PRELIMINARY; PRT; 286 AA.
AC Q20300;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE F4H10.7 protein.
GN F4H10.7
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2004, 15:26:24 ; Search time 23 Seconds
(without alignments)
653.181 Million cell updates/sec

Title: US-09-936-845a-15
Perfect score: 1545
Sequence: 1 MELAEFWNDLNTFTTYGPMH.....PFVKAYIIKSKSKSVKNE 291

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/iaa/5A_COMB.pep:*
4: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
5: /cgn2_6/prodata/2/iaa/PTCUS_COMB.pep:*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	485.5	31.4	278	4	US-09-903-456-58
2	479	31.0	271	4	US-09-903-456-53
3	479	31.0	272	4	US-09-145-828A-18
4	479	31.0	272	4	US-09-903-456-24
5	476.5	30.8	261	4	US-09-903-456-60
6	435.5	28.2	265	4	US-09-903-456-64
7	360	23.3	265	4	US-09-903-456-55
8	360	23.3	265	4	US-09-903-456-89
9	360	23.3	265	4	US-09-903-456-56
10	360	23.3	288	4	US-09-903-456-62
11	327.5	21.2	238	4	US-09-145-828A-13
12	327.5	21.2	238	4	US-09-903-456-20
13	327.5	21.2	278	4	US-09-145-828A-11
14	327.5	21.2	278	4	US-09-903-456-18
15	288	18.6	141	4	US-09-903-456-47
16	280	18.1	147	4	US-09-145-828A-20
17	280	18.1	147	4	US-09-903-456-27
18	262	17.0	345	4	US-09-145-828A-8
19	262	17.0	345	4	US-09-903-456-15
20	239	15.5	276	4	US-09-903-456-37
21	239	15.5	280	4	US-09-149-478-415
22	235	15.2	272	4	US-09-903-456-76
23	233	15.1	272	4	US-09-903-456-75
24	233	15.1	283	4	US-09-903-456-88
25	233	15.1	288	4	US-09-903-456-88
26	233	15.1	292	4	US-09-903-456-82
27	233	15.1	295	4	US-09-903-456-86

28	232	15.0	272	4	US-09-903-456-78	Sequence 78, Appl
29	231	15.0	272	4	US-09-903-456-80	Sequence 80, Appl
30	230	14.9	272	4	US-09-903-456-79	Sequence 79, Appl
31	229	14.8	272	4	US-09-903-456-81	Sequence 81, Appl
32	226	14.6	299	4	US-09-903-456-66	Sequence 66, Appl
33	221.5	14.3	284	4	US-09-903-456-83	Sequence 83, Appl
34	221.5	14.3	292	4	US-09-903-456-35	Sequence 35, Appl
35	221.5	14.3	293	4	US-09-903-456-45	Sequence 45, Appl
36	221.5	14.3	299	4	US-09-903-456-61	Sequence 61, Appl
37	220	14.2	347	1	US-08-249-420-2	Sequence 2, Appl
38	220	14.2	347	2	US-08-737-663-2	Sequence 2, Appl
39	220	14.2	347	4	US-09-145-828A-16	Sequence 16, Appl
40	220	14.2	347	4	US-09-903-456-14	Sequence 14, Appl
41	219	14.2	283	4	US-09-903-456-85	Sequence 85, Appl
42	219	14.2	292	4	US-09-903-456-65	Sequence 65, Appl
43	216	14.0	280	4	US-09-145-828A-21	Sequence 21, Appl
44	216	14.0	280	4	US-09-903-456-28	Sequence 28, Appl
45	216	14.0	286	4	US-09-903-456-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-09-903-456-58
; Sequence 58, Application US/09903456
; Patent No. 6577145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (235)...(235)
; OTHER INFORMATION: Xaa = Unknown or Other at position 235
US-09-903-456-58

Query Match	31.4%	Score	485.5	DB	4	Length	278
Best Local Similarity	37.7%	Pred. No.	3.3e+44				
Matches	103	Conservative	54	Mismatches	99	Indels	17
Gaps	5						
QY	23	MTTKYKSYHPPGQVADP-----QYWTILFQXVYHSHITISVLXFLIKVIOKFMENR	76				
Db	11	VTPNYSYIFDENFDHFHORTKMLENTWTF-YYCGI-----YMLVIFGGQHFMQR	62				
QY	77	KPFTLKVLINWGLAAPSIIATLRFSDPLRSIYAGFYKTLCS--CNPTDVAATWS	134				
Db	63	PRFQLRGFLIIWNTLLAMFSIMGAARTAPELIHVLRHGLFHSVCVPSYIEQDRVCGFWT	122				
QY	135	FAPALSKIVELGDMPFILLRKPLIELHYHHAVALIYTVHSGAHTAAGRFYILMYFA	194				
Db	123	WLFVLSKLPGLDGFIFIVLRKQPLIFLHWHTIIVLIYSWFSTYETSSAFAFWNVCV	182				
QY	195	HSLMYTYTVTSANGYRLPKWYSMTVTVTQTQMLAGVI-TWMYVKVTEYKLPQQQSV	253				

Db 183 HSMVSYALKAAFPNPRFISMIIITSLQALQMIIGCALNVWANGFLKTHGTXSCHISOR 242
QY 254 NLXLAFVIVYTTAILIQFVKAYIITKSKSK 286
Db 243 NNLSTAMYSYVFLPAREFFKAYLAPGGHKS 275

RESULT 2

US-09-903-456-53
; Sequence 53, Application US/09903456
; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-903-456-53

Query Match 31.0%; Score 479; DB 4; Length 271;
Best Local Similarity 41.6%; Pred. No. 1.6e-43;
Matches 101; Conservative 47; Mismatches 87; Indels 8; Gaps 4;
QY 49 QKYNHSTITSVLYFILIKVIOKFMENKPTLKYPLILMNGALAAFSIATLRFSDPL 108
Db 32 EBYWSSFLIVVYLLIIVGQTYMTRKSPSLQRPILMSFFLAIFSLGTLRWKFWA 91
QY 109 RSLVAEGFYKTLVSCNPTD-VAAFWSPAFALSKIVELGDTMFIILKRPLIFLHYHHA 167
Db 92 TWMFTVGLKQIVCPAIYTDADVVRWFSFLSKVVELGDTAFIILKRPLIFVHWYHS 151
QY 168 AVLIYTVHSGAHTAAGRPYILMNYFAHSLMYTYTYSAMGYRLPKVSWMTVTVTQTM 227
Db 152 TVLLFTSFGYKKNKVPSCGFWMTMFGVHSMVYTYTMMKAALKHPNLLPMTVITSLQILQM 211
QY 228 LAGV-GITWVYKVKTEYKLPQOOSVANLYLAFVIVYVTFALFIQFVKAYIISK-K 284
Db 212 VLGTPIGLNYIWR-----QKCGCHTTTEHFFWFSFMLYGTTFILFAHFFHRAYLPRPKVA 267
QY 285 SKS 287
Db 268 SKS 270

RESULT 3

US-09-145-828A-18
; Sequence 18, Application US/09145828A
; Patent No. 6403349
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E. Y.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Kirchner, Stephen J.
; APPLICANT: Parker-Barnes, Jennifer M.
; TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF

; FILE REFERENCE: 6407.US.01
; CURRENT APPLICATION NUMBER: US/09/145,828A
; CURRENT FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (272)...(272)
; OTHER INFORMATION: Xaa = Unknown or other at position 272
US-09-145-828A-18

Query Match 31.0%; Score 479; DB 4; Length 272;
Best Local Similarity 41.6%; Pred. No. 1.6e-43;
Matches 101; Conservative 47; Mismatches 87; Indels 8; Gaps 4;
QY 49 QKYNHSTITSVLYFILIKVIOKFMENKPTLKYPLILMNGALAAFSIATLRFSDPL 108
Db 32 EBYWSSFLIVVYLLIIVGQTYMTRKSPSLQRPILMSFFLAIFSLGTLRWKFWA 91
QY 109 RSLVAEGFYKTLVSCNPTD-VAAFWSPAFALSKIVELGDTMFIILKRPLIFLHYHHA 167
Db 92 TWMFTVGLKQIVCPAIYTDADVVRWFSFLSKVVELGDTAFIILKRPLIFVHWYHS 151
QY 168 AVLIYTVHSGAHTAAGRPYILMNYFAHSLMYTYTYSAMGYRLPKVSWMTVTVTQTM 227
Db 152 TVLLFTSFGYKKNKVPSCGFWMTMFGVHSMVYTYTMMKAALKHPNLLPMTVITSLQILQM 211
QY 228 LAGV-GITWVYKVKTEYKLPQOOSVANLYLAFVIVYVTFALFIQFVKAYIISK-K 284
Db 212 VLGTPIGLNYIWR-----QKCGCHTTTEHFFWFSFMLYGTTFILFAHFFHRAYLPRPKVA 267
QY 285 SKS 287
Db 268 SKS 270

RESULT 4

US-09-903-456-24
; Sequence 24, Application US/09903456
; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (272)...(272)
; OTHER INFORMATION: Xaa = Unknown or Other at position 272
US-09-903-456-24

Query Match 31.0%; Score 479; DB 4; Length 272;

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Best Local Similarity 41.6%; Pred. No. 1.6e-43;
Matches 101; Conservative 47; Mismatches 87; Indels 8; Gaps 4;

QY 49 OKYVHSITISVLKILKQKMNKPTLKYPLILWNGALAAFSIIATLRFSDPL 108
Db 32 EYVWSFLIVVYLLLVGQYMKTRKSLQRLDLSFFLAIFSLTLRWKPKMA 91
QY 109 RSLVAGFYKTLCKSCNPTD--VAAFWSAFALSKIVELGDTMFIILRKRPLIFLHYHHA 167
Db 92 TWMTVLGLKQVCFAYITDDAVREWSFLFLSKVVELGDTAFILRKRPLIFVHWYHHS 151
QY 168 AVLIYVHSAGHTAAGFYILMNPVPAHSLMYTVTVSANGYRLPKWVMTVTTOTOM 227
Db 152 TLLFTSFGYKXKXKSGWFMFMFVHSHVMTYITMKAAKULGNLPLPMTSLQILQM 211
QY 228 LAGV--GITWVYKVKTEYKPLCCQSVANLAFVIYVTFAILFIQFFVKAYIIKSSK-K 284
Db 212 VIGTIFGILNIWR---QKGGCHTTEHFWSEFWLYGTYPILFAHFFHRAVLRPKGVA 267
QY 285 SKS 287
Db 268 SKS 270

RESULT 5
US-09-903-456-60
; Sequence 60, Application US/09903456
; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US 09/903,456
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR FILING DATE: 1999-08-23
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; NAME/KEY: VARIANT
; LOCATION: (218)...(218)
; OTHER INFORMATION: Xaa = Unknown or Other at position 218
US-09-903-456-60

Query Match 30.8%; Score 476.5; DB 4; Length 261;
Best Local Similarity 40.2%; Pred. No. 2.8e-43;
Matches 99; Conservative 49; Mismatches 87; Indels 11; Gaps 4;

QY 44 WTILFKYVHSITISVLKILKQKMNKPTLKYPLILWNGALAAFSIIATLRF 103
Db 21 WTWVF---FYCGI-----YMLVIFGQHEMQRPQLRGPLIIWTLAMFSINGAART 72
QY 104 SIDPLRSLVAGFYKTLCKYS--CNPTDVAAFWSAFALSKIVELGDTMFIILRKRPLIFL 161
Db 73 APELHVLRYHGLFHSVCVPSIEQDRVCGFTWLVLSKLPGLDTPVLRKQPLIFL 132
QY 162 HYHHAVALIYVHSGAHTAAGFYILMNPVPAHSLMYTVTVSANGYRLPKWVMTVT 221
Db 133 HWYHHTVLIYSFSTYETSSARFVIMNVCVHSYVYALKAAAREPNPPEFSMILTS 192
QY 222 VQTQMLAGVGI-TWVYKVKTEYKPLCCQSVANLAFVIYVTFAILFIQFFVKAYIIK 280
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Db 193 LQLAQMTIGCAINWANGFLKTHGTXSCHISQORNILSIAMYSYFVLFARFFYKAYLAP 252
QY 281 SSKSK 286
Db 253 GGHKS 258

RESULT 6
US-09-903-456-64
; Sequence 64, Application US/09903456
; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US 09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-903-456-64

Query Match 28.2%; Score 435.5; DB 4; Length 265;
Best Local Similarity 35.8%; Pred. No. 7.5e-39;
Matches 95; Conservative 54; Mismatches 103; Indels 13; Gaps 5;

QY 26 KYKSYHFPGEQVADPOYWTILFKYVHSITISVLKILKQKMNKPTLKYPL 85
Db 10 EYFEKQFNENEAIQ---W---MOENWKQSFLFSALYAAFPGRHLMYKGAKELRKPL 63
QY 86 ILWNGALAAFSIIATLRFSDPLRSLVAGFYKTLCK---YSCNPTDVAAFWSAFALSKI 142
Db 64 VLWSLTAVFSIFCALRTGAYMVYILATKGLKQSCVCDQGFYNGP--VSKFWAYAFVLSKA 121
QY 143 VELGDTMFIILRKRPLIFLHYHHAVALIYVHSGAHTAAGFYILMNPVPAHSLMYTY 202
Db 122 PELGDTTIFILRKQKILFLHWYHHTITVLLYSWYSYKDWAGGWMFTMNYGVHAWMSYI 181
QY 203 TVSAMGYRLPKWVMTVTVTQTTQMLAGVGIWVYKVKTEYKPLCCQSVANLAFVIY 262
Db 182 ALRANGFVSRKFAFNTLSQITQMLMGCVNVLVFCWMOHQDQ--CHSHFQNIWFSSLMY 239
QY 263 VTFAILFIQFFVKAYTIKSSKUS 287
Db 240 LSYLVLFCHFFFEAYIGDRXTTKA 264

RESULT 7
US-09-903-456-55
; Sequence 55, Application US/09903456
; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
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; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-09-903-456-55

Query Match      23.3%; Score 360; DB 4; Length 265;
Best Local Similarity 31.3%; Pred. No. 1e-30;
Matches 76; Conservative 58; Mismatches 107; Indels 2; Gaps 2;

QY 48 FQKYWYHSITISLVYFILIKVIOKFMENKRPFTLKYPILMNGALAAFSIIATLRFSDP 107
DB 17 FADHFDVTIOASILYMWVVFQKWFENRQPPQLTIPLINMNFILAAFSIAGAVKMTPEF 76
QY 108 LRSIYABGFYKTLGYSCNPT-DVAAFSPAPALS KIVELGDTMFIILRKRPLIFLHYHH 166
DB 77 FGTIANKGIVASYCKVDFDTKGNGYWWLFWASKL FELVDITFLVLRKPLMFLHWYH 136
QY 167 AAVLIYTVHSGAEHTAAGFYILMNYFAHSLMYTYTYSAMGYRLPKWVSMVTVTQTQ 226
DB 137 ILTMIVAWYSHPLTPGFNRYGIYLFVWFAFMYSYFLSRMKIRVPGFIAQAITSIQIVQ 196
QY 227 MLAGVGITWVYKVKTEYKLPQOOSVANLYLAFVIYVTFAILFIOPFVKAYIIKSSK-KS 285
DB 197 FIISCAVLAHLGYLMHFTNANCDPEPSVFKLAVFMDTTIYALFVNFLOSYVLRGGDKY 256
QY 286 KSV 288
DB 257 KAV 259

RESULT 9
US-09-903-456-56
; Sequence 56, Application US/09903456
; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Bun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407 US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-09-903-456-56

Query Match      23.3%; Score 360; DB 4; Length 288;
Best Local Similarity 31.3%; Pred. No. 1e-30;
Matches 76; Conservative 58; Mismatches 107; Indels 2; Gaps 2;

QY 48 FQKYWYHSITISLVYFILIKVIOKFMENKRPFTLKYPILMNGALAAFSIIATLRFSDP 107
DB 40 FADHFDVTIOASILYMWVVFQKWFENRQPPQLTIPLINMNFILAAFSIAGAVKMTPEF 99
QY 108 LRSIYABGFYKTLGYSCNPT-DVAAFSPAPALS KIVELGDTMFIILRKRPLIFLHYHH 166
DB 100 FGTIANKGIVASYCKVDFDTKGNGYWWLFWASKL FELVDITFLVLRKPLMFLHWYH 159
QY 167 AAVLIYTVHSGAEHTAAGFYILMNYFAHSLMYTYTYSAMGYRLPKWVSMVTVTQTQ 226
DB 160 ILTMIVAWYSHPLTPGFNRYGIYLFVWFAFMYSYFLSRMKIRVPGFIAQAITSIQIVQ 219
QY 227 MLAGVGITWVYKVKTEYKLPQOOSVANLYLAFVIYVTFAILFIOPFVKAYIIKSSK-KS 285
DB 220 FIISCAVLAHLGYLMHFTNANCDPEPSVFKLAVFMDTTIYALFVNFLOSYVLRGGDKY 279
QY 286 KSV 288
DB 280 KAV 282
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; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-09-903-456-55

Query Match      23.3%; Score 360; DB 4; Length 265;
Best Local Similarity 31.3%; Pred. No. 1e-30;
Matches 76; Conservative 58; Mismatches 107; Indels 2; Gaps 2;

QY 48 FQKYWYHSITISLVYFILIKVIOKFMENKRPFTLKYPILMNGALAAFSIIATLRFSDP 107
DB 17 FADHFDVTIOASILYMWVVFQKWFENRQPPQLTIPLINMNFILAAFSIAGAVKMTPEF 76
QY 108 LRSIYABGFYKTLGYSCNPT-DVAAFSPAPALS KIVELGDTMFIILRKRPLIFLHYHH 166
DB 77 FGTIANKGIVASYCKVDFDTKGNGYWWLFWASKL FELVDITFLVLRKPLMFLHWYH 136
QY 167 AAVLIYTVHSGAEHTAAGFYILMNYFAHSLMYTYTYSAMGYRLPKWVSMVTVTQTQ 226
DB 137 ILTMIVAWYSHPLTPGFNRYGIYLFVWFAFMYSYFLSRMKIRVPGFIAQAITSIQIVQ 196
QY 227 MLAGVGITWVYKVKTEYKLPQOOSVANLYLAFVIYVTFAILFIOPFVKAYIIKSSK-KS 285
DB 197 FIISCAVLAHLGYLMHFTNANCDPEPSVFKLAVFMDTTIYALFVNFLOSYVLRGGDKY 256
QY 286 KSV 288
DB 257 KAV 259

RESULT 8
US-09-903-456-89
; Sequence 89, Application US/09903456
; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Bun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407 US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-09-903-456-89

Query Match      23.3%; Score 360; DB 4; Length 265;
Best Local Similarity 31.3%; Pred. No. 1e-30;
Matches 76; Conservative 58; Mismatches 107; Indels 2; Gaps 2;
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```
RESULT 10
US-09-903-456-62
; Sequence 62, Application US/09903456
; Patent No. 6677145
; ORGANISM: Caenorhabditis elegans
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-903-456-62

Query Match      23.3%; Score 360; DB 4; Length 288;
Best Local Similarity 31.3%; Pred. No. 1.1e-30;
Matches 76; Conservative 58; Mismatches 107; Indels 2; Gaps 2;

QY 48 FQKYVHSTISVLYFILIKVQKFMENRKPTLKYPILMNGALAAFSIIATLRFSDP 107
Db 40 FADHDVDTIQASILYVGVFGTKWENRNPQFPQLTPLNINWIFLAAFSAGAVKPTPEF 99
QY 108 LRSLYAEGFYKTLCSNPT-DVAAPFSPAFALSKIVELGDTMFIILRKRPILFLHYHH 166
Db 100 FGTIANKGIVASVCKYFDFTKGNGYVWLFNASKLPFLVDITFLVLRKPLMFLRWYHH 159
QY 167 AAVLYTVHSGAHTAAGRFYILMNYFAHSLMYTYTVTSAMGYRLPKWVMTVTVTQT 226
Db 160 ILTIMIYAMVSHLTPGPNRYGYLNFVHAFFMYSYFLSKIRVPGFIAQAITSLQIVQ 219
QY 227 MLAGVGITMWMYKVKTKYKLPQOQSANLYLAFVIYVTFALIFIOFFVKAYIKSK-KS 285
Db 220 FIISCAVLAHLGYLMFTNANDPEPSVFKLAVFMDTTLALFVNFQSVLRGCKDY 279
QY 286 KSV 288
Db 280 KAV 282

RESULT 11
US-09-145-828A-13
; Sequence 13, Application US/09145828A
; Patent No. 6403349
; ORGANISM: Caenorhabditis elegans
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E. Y.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Kirchner, Stephen J.
; APPLICANT: Parker-Barnes, Jennifer M.
; TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
; FILE REFERENCE: 6407.US.01
; CURRENT APPLICATION NUMBER: US/09/145,828A
; CURRENT FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
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; LENGTH: 238
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-145-828A-13

Query Match      21.2%; Score 327.5; DB 4; Length 238;
Best Local Similarity 33.9%; Pred. No. 2.8e-27;
Matches 75; Conservative 46; Mismatches 91; Indels 9; Gaps 6;

QY 49 QKYVHSTISVLYFILIKVQKFMENRKPTLKYPILMNGALAAFSIIAT---LRFSI 105
Db 20 QEFGCLFVQMAIAYVILVFSIKRPMRDREPPQLTALTALRNWFFLSVFSIYGSWTMFPFMV 79
QY 106 DPLRSLYAEGFYKTLCSY-CNPTDVAAPFSPAFALSKIVELGDTMFIILRKRPILFLHY 164
Db 80 QQIR-LY--GLYGCCEALSNLPSQAEYWLFTLISKAVEFVDFTFLLVRKPKPLFLHY 136
QY 165 HAAVLYTVHSGAHTAAGRFYILMNYFAHSLMYTYTVTSAMGYRLPKWVMTVTVTQT 224
Db 137 HMAITVFFCSNYPTPSSQSRVGVINLVFAFMYPPYFTSMNKKVPKISMATVTLQL 196
QY 225 TOMLAGV-GITMWMYKVKTK-BYKLPQOQSANLYLAFVIYV 263
Db 197 TQFMCFIYGCTLMYSLATNQARYPSNTPATLQCLSVTLHL 237

RESULT 12
US-09-903-456-20
; Sequence 20, Application US/09903456
; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-903-456-20

Query Match      21.2%; Score 327.5; DB 4; Length 238;
Best Local Similarity 33.9%; Pred. No. 2.8e-27;
Matches 75; Conservative 46; Mismatches 91; Indels 9; Gaps 6;

QY 49 QKYVHSTISVLYFILIKVQKFMENRKPTLKYPILMNGALAAFSIIAT---LRFSI 105
Db 20 QEFGCLFVQMAIAYVILVFSIKRPMRDREPPQLTALTALRNWFFLSVFSIYGSWTMFPFMV 79
QY 106 DPLRSLYAEGFYKTLCSY-CNPTDVAAPFSPAFALSKIVELGDTMFIILRKRPILFLHY 164
Db 80 QQIR-LY--GLYGCCEALSNLPSQAEYWLFTLISKAVEFVDFTFLLVRKPKPLFLHY 136
QY 165 HAAVLYTVHSGAHTAAGRFYILMNYFAHSLMYTYTVTSAMGYRLPKWVMTVTVTQT 224
Db 137 HMAITVFFCSNYPTPSSQSRVGVINLVFAFMYPPYFTSMNKKVPKISMATVTLQL 196
QY 225 TOMLAGV-GITMWMYKVKTK-BYKLPQOQSANLYLAFVIYV 263
Db 197 TQFMCFIYGCTLMYSLATNQARYPSNTPATLQCLSVTLHL 237
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RESULT 13
US-09-145-828A-13
; Sequence 13, Application US/09145828A
; Patent No. 6403349
; ORGANISM: Caenorhabditis elegans
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E. Y.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Kirchner, Stephen J.
; APPLICANT: Parker-Barnes, Jennifer M.
; TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
; FILE REFERENCE: 6407.US.01
; CURRENT APPLICATION NUMBER: US/09/145,828A
; CURRENT FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
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```
RESULT 13
US-09-145-828A-11
; Sequence 11, Application US/09145828A
; Patent No. 6403349
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Ananda B. Y.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Thurmond, Jennifer J.
; APPLICANT: Kirchner, Stephen J.
; APPLICANT: Parker-Barnes, Jennifer M.
; TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
; FILE REFERENCE: 6407.US.01
; CURRENT APPLICATION NUMBER: US/09/145,828A
; CURRENT FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-145-828A-11

Query Match      21.2%; Score 327.5; DB 4; Length 278;
Best Local Similarity 32.8%; Pred. No. 3.5e-27;
Matches 80; Conservative 44; Mismatches 109; Indels 11; Gaps 6;

QY 55 SITISVLVFLIKVIOKFNENKPTLKYPLILNGLAALAFSIIATLRSIDPLRS-LYA 113
Db 30 SAKLAVGIATIFGLKYMKDKRKAFLDSTPLNINWILSTFSLGL-FTFPTLLSVIRK 88
QY 114 EGFYKTLCY--SCNPTDVAAPFAPALSIVELGDTMFIILKRPLIFLHYHAAVLI 171
Db 89 DGFSTYSHVSELYTDSGTGYWIFLVWISKIPELLDTVFLVLRKPLIFMEWHYHALTCY 148
QY 172 YTV---HSGAEHTAGRFILMYFAHSLMYTYTVTSANGYRLPKWVMTVTVTQML 228
Db 149 YALVCYHEDAVHMV---WVWMNYIIHAFMYGYLLSKLKVPIPPSVAQAITSQMVQFA 205
QY 229 AGV-GITMVMYKVKTEYKLPQQQSVANLYLAFVIYVTFAILFIQFVKAYIIKSKSKS 287
Db 206 VAIFAQVHSYKHVYEGVEGLAYSFRGTAIGFMTTYFYLWIQFYKHYLANGGKKYNL 265
QY 288 VKNE 291
Db 266 AKDQ 269

RESULT 14
US-09-903-456-18
; Sequence 18, Application US/09903456
; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Ananda B. Y.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: VARIANT
; LOCATION: (141)...(141)
; OTHER INFORMATION: Xaa = Unknown or Other at position 141
US-09-903-456-18

Query Match      18.6%; Score 288; DB 4; Length 141;
Best Local Similarity 39.0%; Pred. No. 2.5e-23;
Matches 55; Conservative 36; Mismatches 48; Indels 2; Gaps 1;

QY 147 DTMFIILKRKPLIFLHYHAAVLIYTVHSGAEHTAGRFILMYFAHSLMYTYTVTSA 206
Db 1 DTFIILKRKQKLIIFLHYHAAVLIYTVHSGAEHTAGRFILMYFAHSLMYTYTVTSA 60
QY 207 MGYRLPKWVMTVTVTQMLAGVITMVKYKTEYKLPQQQSVANLYLAFVIYVTF 266
```

```
; SEQ ID NO 18
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-903-456-18

Query Match      21.2%; Score 327.5; DB 4; Length 278;
Best Local Similarity 32.8%; Pred. No. 3.5e-27;
Matches 80; Conservative 44; Mismatches 109; Indels 11; Gaps 6;

QY 55 SITISVLVFLIKVIOKFNENKPTLKYPLILNGLAALAFSIIATLRSIDPLRS-LYA 113
Db 30 SAKLAVGIATIFGLKYMKDKRKAFLDSTPLNINWILSTFSLGL-FTFPTLLSVIRK 88
QY 114 EGFYKTLCY--SCNPTDVAAPFAPALSIVELGDTMFIILKRPLIFLHYHAAVLI 171
Db 89 DGFSTYSHVSELYTDSGTGYWIFLVWISKIPELLDTVFLVLRKPLIFMEWHYHALTCY 148
QY 172 YTV---HSGAEHTAGRFILMYFAHSLMYTYTVTSANGYRLPKWVMTVTVTQML 228
Db 149 YALVCYHEDAVHMV---WVWMNYIIHAFMYGYLLSKLKVPIPPSVAQAITSQMVQFA 205
QY 229 AGV-GITMVMYKVKTEYKLPQQQSVANLYLAFVIYVTFAILFIQFVKAYIIKSKSKS 287
Db 206 VAIFAQVHSYKHVYEGVEGLAYSFRGTAIGFMTTYFYLWIQFYKHYLANGGKKYNL 265
QY 288 VKNE 291
Db 266 AKDQ 269
```

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RESULT 15
US-09-903-456-47
; Sequence 47, Application US/09903456
; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Ananda B. Y.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: VARIANT
; LOCATION: (141)...(141)
; OTHER INFORMATION: Xaa = Unknown or Other at position 141
US-09-903-456-47
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Query Match      18.6%; Score 288; DB 4; Length 141;
Best Local Similarity 39.0%; Pred. No. 2.5e-23;
Matches 55; Conservative 36; Mismatches 48; Indels 2; Gaps 1;

QY 147 DTMFIILKRKPLIFLHYHAAVLIYTVHSGAEHTAGRFILMYFAHSLMYTYTVTSA 206
Db 1 DTFIILKRKQKLIIFLHYHAAVLIYTVHSGAEHTAGRFILMYFAHSLMYTYTVTSA 60
QY 207 MGYRLPKWVMTVTVTQMLAGVITMVKYKTEYKLPQQQSVANLYLAFVIYVTF 266
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Db 61 AGFRVSRKFPAMFTLSQITQMLMGCVVNYLVFCWMOHQDQ-CHSHFQNIWFSSLMYLSYL 118

QY 267 ILFIQPFVKAYILKSSKKS 287

Db 119 VLFCHFFFEAYIGMRKTKA 139

Search completed: June 16, 2004, 15:30:08
Job time : 24 secs